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ON protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 42.7959 Seconds
(without alignments)
118.840 Million cell updates/sec

Title: US-10-084-813-11

Perfect score: 94

Sequence: 1 LPFLSLVFIFGFVGNWL 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1980s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	18	4	AAB88916
2	94	100.0	18	4	AAB88931
3	94	100.0	27	2	AAW33994
4	94	100.0	27	2	AAW33961
5	94	100.0	29	2	AAW40023
6	94	100.0	83	2	AAW01249
7	94	100.0	100	2	AAW88231
8	94	100.0	184	2	AAW27406
9	94	100.0	215	2	AAW27408
10	94	100.0	215	2	AAW88238
11	94	100.0	329	4	AAW46859
12	94	100.0	329	5	ABE81055
13	94	100.0	332	2	AAW26766
14	94	100.0	344	5	ABG92881
15	94	100.0	344	6	ABU61655
16	94	100.0	352	2	AAW27407
17	94	100.0	352	2	AAW27123
18	94	100.0	352	2	AAW07602
19	94	100.0	352	2	AAW23835
20	94	100.0	352	2	AAW88232
21	94	100.0	352	3	AAW80128
22	94	100.0	352	4	AAW9089
23	94	100.0	352	4	AAW07046
24	94	100.0	352	4	AAW07048
25	94	100.0	352	4	AAW80111

26	94	100.0	352	4	AAE04321	Aae04321 Human che
27	94	100.0	352	4	AAE07037	Aae07037 Human G-p
28	94	100.0	352	4	AAE07039	Aae07039 Human G-p
29	94	100.0	352	4	AB46858	Ab46858 Human HDG
30	94	100.0	352	4	AB56342	Ab56342 Nori-endog
31	94	100.0	352	4	AB83354	Ab83354 Human CCR
32	94	100.0	352	4	AB82948	Ab82948 Human HIV
33	94	100.0	352	5	AAU97150	Aau97150 Human G-p
34	94	100.0	352	5	AAU97152	Aau97152 Human G-p
35	94	100.0	352	5	AAU52829	Aam52829 Human CCR
36	94	100.0	352	5	AAU52828	Aam52828 Human CC
37	94	100.0	352	5	ABG70597	Abg70597 Human G-p
38	94	100.0	352	5	ABG92883	Abg92883 Human imm
39	94	100.0	352	5	ABG92880	Abg92880 Human G-p
40	94	100.0	352	5	AAE25808	Aae25808 Human G-p
41	94	100.0	352	5	AAE25811	Aae25811 Human G-p
42	94	100.0	352	5	AB81054	Abb81054 G-protein
43	94	100.0	352	5	AB80843	Abb08343 Human che
44	94	100.0	352	6	ABG75540	Abg75540 Human G-p
45	94	100.0	352	6	ABR58602	Abf58602 Human can
46	94	100.0	352	6	AAO29514	Aao29514 Human C-C
47	94	100.0	352	6	ABU61654	Abu61654 Human G-p
48	94	100.0	352	6	ABP97728	Abp97728 Amino aci
49	94	100.0	352	6	ABP81933	Abp81933 Human C-C
50	94	100.0	352	7	ADC03341	Adc03341 Human che
51	94	100.0	360	2	AAU79166	Aar79166 Human mon
52	94	100.0	360	2	AAW35833	Aaw35833 Human mon
53	94	100.0	360	2	AAW80108	Aag80108 Human CCR
54	94	100.0	360	4	AAU07613	Aau07613 Human CCR
55	94	100.0	360	4	AAU07614	Aau07614 Human wil
56	94	100.0	360	4	ABR56340	Abb56340 Non-endog
57	94	100.0	360	6	ABP97725	Abp97725 Amino aci
58	94	100.0	360	6	ABP81987	Abp81987 Human C-C
59	94	100.0	371	2	AAW23834	Aaw23834 Human CC
60	94	100.0	374	2	AAU79165	Aar79165 Human mon
61	94	100.0	374	6	AAW80107	Aag80107 Human CCR
62	94	100.0	374	6	ABU09083	Abu09083 Human che
63	94	100.0	374	7	ADD44861	Adg44861 Human Pro
64	94	100.0	374	7	ADD44865	Adg44865 Human Pro
65	94	100.0	439	2	AAU41280	Aay41280 Fusion pr
66	92	97.9	354	7	ADD44859	Add44859 Rat Prote
67	92	97.9	354	7	ADD44863	Add44863 Rat Prote
68	90	95.7	268	7	ADC10142	Adc10142 Human NOV
69	90	95.7	268	7	ADC10144	Adc10144 Human NOV
70	90	95.7	352	7	AAW27125	Aaw27125 Macaque c
71	90	95.7	352	7	ADC03359	Adc03359 Mouse CC-
72	88	93.6	354	2	AAW54037	Aaw54037 Mouse CC-
73	77	81.9	31	2	AAW39995	Aaw39995 Peptide e
74	77	81.9	355	2	AAE52749	Aar52749 C-C chemo
75	77	81.9	355	2	AAW25751	Aaw25751 Human MIP
76	77	81.9	355	2	AAW26588	Aaw26588 Human MIP
77	77	81.9	355	3	AAW20571	Aab20571 Human CC-
78	77	81.9	355	6	ABU09082	Abu09082 Human che
79	77	81.9	355	6	ABP97724	Abp97724 Amino aci
80	77	81.9	355	6	ABP81790	Abp81790 Human C-C
81	75	79.8	360	2	AAU99274	Aar99274 Chemokine
82	75	79.8	360	3	AAW07498	Aab07498 A human C
83	75	79.8	360	4	AAW80110	Aag80110 Human CCR
84	75	79.8	360	4	AAW80111	Aag80111 Human CCR
85	75	79.8	360	6	ABR40283	Abf40283 Human ami
86	75	79.8	360	6	ABU09085	Abu09085 Human che
87	75	79.8	360	6	ABP97727	Abp97727 Amino aci
88	75	79.8	360	6	ABP81792	Abp81792 Human C-C
89	75	79.8	360	7	ADE27676	Adc27676 Human seq
90	75	79.8	361	4	ABB11966	Abb11966 Human CCR
91	73	77.7	18	4	AB88915	Ab88915 HIV gp120
92	73	77.7	355	2	AAW29179	Aaw29179 Rat CC ch
93	73	77.7	355	7	ADD45360	Add45360 Rat Prote
94	72	76.6	18	4	AB88917	Ab88917 HIV gp120
95	70	74.5	355	2	AAW51744	Aaw51744 Human C-C
96	67	71.3	13	2	AAW33968	Aaw33968 CCR5 rece
97	63	67.0	332	5	ABJ03698	Abj03698 Human ova
98	63	67.0	355	2	AAW03376	Aaw03376 CC-chemok

99 63 67.0 355 2 AAW03377 CC-Chemok
100 63 67.0 355 2 AAW03378 CC-Chemok

ALIGNMENTS

RESULT 1

AAB88916
ID AAB88916 standard; peptide; 18 AA.
AC AAB88916;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #9.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.
XX
PS Claim 21; Page 38; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 94; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
DB 1 LPPLYSLVFIFGVGNML 18

RESULT 2

AAB88993
ID AAB88993 standard; peptide; 18 AA.
AC AAB88993;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #86.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.

Query Match 100.0%; Score 94; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
DB 1 LPPLYSLVFIFGVGNML 18

RESULT 2

AAB88993
ID AAB88993 standard; peptide; 18 AA.
AC AAB88993;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #86.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.

XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US023505.
XX
XX 27-AUG-1999; 99US-0151270P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX and binds to HIV gp120 under physiological conditions.
XX
XX Claim 21; Page 38; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
XX bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX useful in the treatment of HIV, as they prevent replication of the virus.
XX The present sequence is an example of a peptide of the invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 94; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
DB 1 LPPLYSLVFIFGVGNML 18

RESULT 3

AAB33994
ID AAB33994 standard; peptide; 27 AA.
XX
XX AAB33994;
XX
DT 28-MAY-1998 (first entry)
XX
XX CCR5 receptor antagonist.
XX
KW Antagonist; integral membrane protein; inhibitor; transmembrane domain;
KW therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
KW post-myocardial infarction; HIV infection; cell proliferation disorder;
KW peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
KW antibacterial; CCR5 receptor.
XX
XX Homo sapiens.
XX
XX WO9735881-A2.
XX
XX

PD 02-OCT-1997.

PF 26-MAR-1997; 97WO-CA000203.
XX
XX 27-NAR-1996; 96US-0014306P.
XX
XX 25-JUN-1996; 96US-00670119.
XX
XX 20-AUG-1996; 96US-0024240P.
XX
XX (NGGY/) NG G Y K.
XX (SEEM/) SEEMAN P.
XX (GEOR/) GEORGE S R.
XX (ODOW/) O'DOWD B F.
XX
XX Ng GYK, Seeman P, George SR, Odowd BF;
XX

DR WPI; 1997-489566/45.
 XX Inhibitor of integral membrane protein - used to treat e.g.
 PT schizophrenia, hypertension, viral infection, cancer etc.
 XX Disclosure; Page 88; 127pp; English.
 XX
 CC This sequence represents a CCR5 receptor antagonist, and is an antagonist
 CC of the invention. The antagonists (A) are for inhibiting the function of
 CC a prokaryotic or eukaryotic integral membrane protein (IMP) having at
 CC least one transmembrane domain (TMD), comprises a peptide including at
 CC least 4 consecutive amino acids (aa) from the sequence of the TMD. (A)
 CC are used to treat or prevent disorders in mammals that involve
 CC disturbances of IMP, and the same effect is achieved by inserting a
 CC nucleic acid encoding (A) into the cells of the mammal. Specified
 CC conditions that can be treated are schizophrenia, psychotic disorders,
 CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
 CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
 CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
 CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
 CC renal disease, Parkinson's disease, congestive heart failure, migraine,
 CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
 CC diseases, graft rejection etc. (A) can be used as diuretics and
 CC antibacterials. (A) may also be used to determine function of orphan
 CC receptors and, when attached to a marker, for tissue imaging to
 CC localise/quantify specific receptors. The transgenic animals are used to
 CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
 CC specific and selective, against the IMP from which they are derived, so
 CC should have few side effects
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 94; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIPIFGVGNML 18
 Db 2 LPPLSLVFIPIFGVGNML 19
 RESULT 4
 ID AAW33961 standard; peptide; 27 AA.
 AC AAW33961;
 DT 28-MAY-1998 (first entry)
 DE CCR5 receptor antagonist.
 XX Antagonist; integral membrane protein; inhibitor; transmembrane domain;
 KW therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
 KW post-myocardial infarction; HIV infection; cell proliferation disorder;
 KW peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
 KW antibacterial; CCR5 receptor.
 XX
 OS Homo sapiens.
 XX W09735881-A2.
 FN 02-OCT-1997.
 PD 26-MAR-1997; 97WO-CA000203.
 XX 27-MAR-1996; 96US-0014306P.
 PR 25-JUN-1996; 96US-00670119.
 PR 20-AUG-1996; 96US-0024240P.
 XX (NGY//) NG G Y K.
 PA (SEEM//) SEEMAN P.
 PA (GEOR//) GEORGE S R.
 PA (ODOW//) O'DOWD B F.

XX Ng GYK, Seeman P, George SR, Odowd BF;
 XX WPI; 1997-489566/45.
 XX Inhibitor of integral membrane protein - used to treat e.g.
 PT schizophrenia, hypertension, viral infection, cancer etc.
 XX Claim 22; Page 96; 127pp; English.
 XX This sequence represents a CCR5 receptor antagonist, and is an antagonist
 CC of the invention. The antagonists (A) are for inhibiting the function of
 CC a prokaryotic or eukaryotic integral membrane protein (IMP) having at
 CC least one transmembrane domain (TMD), comprises a peptide including at
 CC least 4 consecutive amino acids (aa) from the sequence of the TMD. (A)
 CC are used to treat or prevent disorders in mammals that involve
 CC disturbances of IMP, and the same effect is achieved by inserting a
 CC nucleic acid encoding (A) into the cells of the mammal. Specified
 CC conditions that can be treated are schizophrenia, psychotic disorders,
 CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
 CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
 CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
 CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
 CC renal disease, Parkinson's disease, congestive heart failure, migraine,
 CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
 CC diseases, graft rejection etc. (A) can be used as diuretics and
 CC antibacterials. (A) may also be used to determine function of orphan
 CC receptors and, when attached to a marker, for tissue imaging to
 CC localise/quantify specific receptors. The transgenic animals are used to
 CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
 CC specific and selective, against the IMP from which they are derived, so
 CC should have few side effects
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 94; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIPIFGVGNML 18
 Db 2 LPPLSLVFIPIFGVGNML 19
 RESULT 5
 ID AAW40023 standard; peptide; 29 AA.
 AC AAW40023;
 DT 18-JUN-1998 (first entry)
 DE Peptide effecting G-protein-coupled receptor activity.
 XX G-protein-coupled receptor; GPCR; transmembrane domain; oligomerisation;
 KW therapeutic composition; GPCR function; receptor monomeric form;
 KW multimeric form; inhibition; GPCR-mediated process; GPCR binding;
 KW treatment; disease.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX W09800538-A2.
 PN 08-JAN-1998.
 XX 01-JUL-1997; 97WO-IB000814.
 PR 01-JUL-1996; 96US-0021031P.
 XX (BIOS-) BIOSIGNAL INC.
 PA (UTMO-) UNIV MONTREAL.

PI Bouvier M, Dennis M, Hebert TE;
 XX WPI; 1998-086964/08.
 XX
 XX Peptide(s) or peptide leads affecting G protein-coupled receptor activity
 PT - by altering receptor oligomerisation, useful in, e.g. selectively
 PT modulating receptor function and treating neurological or genetic
 PT diseases.
 XX
 XX Claim 20; Page 63; 75pp; English.
 XX
 XX Peptides AA040023-29 are modelled on transmembrane domains one to seven,
 CC respectively, of chemokine CC CR5, a G-protein-coupled receptor (GPCR)
 CC (sac) whose activity is affected by the formation of oligomers. GPCRs
 CC have a recurring pattern unique for the transmembrane domains. The
 CC peptides are characterised by the ability to selectively affect
 CC oligomerisation of the GPCR from which it was designed. The peptides may
 CC be used with suitable carriers in the preparation of therapeutic
 CC compositions. They may be administered to selectively modulate GPCR
 CC function by affecting the ratio of receptor monomeric to multimeric
 CC forms. The compositions can be administered to inhibit GPCR-mediated
 CC processes by modulating GPCR binding to its agonist or antagonist. The
 CC peptides may also be used to prevent or treat diseases involving GPCRs.
 CC They are also useful for in vitro and in vivo studies of GPCRs.
 XX
 XX SQ Sequence 29 AA;
 Query Match 100.0%; Score 94; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIQFGVGNML 18
 Db 6 LPPLYSLVFIQFGVGNML 23
 |||||
 RESULT 6
 AA01249
 ID AA01249 standard; protein; 83 AA.
 AC
 XX
 XX AA01249;
 XX
 XX 28-MAY-1999 (first entry)
 XX
 XX Chemokine receptor CCR2 mutant allele CCR2-64I protein sequence.
 XX
 XX HIV; chemokine; co-receptor; CCR2; mutant; AIDS; CCR2-64I; asthma;
 KW inflammatory response; arthritis; Crohn's disease; Grave's disease;
 KW lupus; pulmonary disease; cystic fibrosis.
 XX
 XX Human immunodeficiency virus 1.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 64
 FT /label= V64I
 FT /note= "wild-type Val is replaced by Ile"
 XX
 XX WO9909162-A2.
 XX
 XX 25-FEB-1999.
 XX
 XX 10-AUG-1998; 98WO-US016523.
 XX
 XX 14-AUG-1997; 97US-0055659P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Dean M, O'Brien SJ, Smith M, Carrington M;
 XX WPI; 1999-190162/16.
 XX
 XX A new CCR2 chemokine receptor, CCR2-64I - useful to delay AIDS

PT progression.
 XX
 XX Claim 11; Page; 72pp; English.
 XX
 XX The invention relates to a new allele of an HIV co-receptor, CCR2, having
 CC isoleucine substituted for valine at position 64, which delays AIDS
 CC progression in HIV-infected individuals. Host cells containing a vector
 CC comprising the nucleic acid encoding the mutant allele CCR2-64I are used
 CC for the recombinant expression of the mutant. The molecules of the
 CC invention are used to treat diseases associated with HIV infection, or
 CC those characterised by an inflammatory response, including asthma,
 CC arthritis, Crohn's disease, lupus, Grave's disease, and pulmonary disease
 CC associated with cystic fibrosis. The present sequence represents the
 CC amino acid sequence of the mutant allele CCR2-64I. Note: This sequence is
 CC not provided in the specification. It has been created by modifying the
 CC wild-type CCR2 sequence provided in Fig 1
 XX
 XX SQ Sequence 83 AA;
 Query Match 100.0%; Score 94; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIQFGVGNML 18
 Db 45 LPPLYSLVFIQFGVGNML 62
 |||||
 RESULT 7
 AA08231
 ID AA08231 standard; protein; 100 AA.
 AC
 XX
 XX AA08231;
 XX
 XX 15-MAR-1999 (first entry)
 XX
 XX HIV-1 co-receptor CCR5 variant CCR5m303.
 DE
 XX HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Domain 32..56
 FT /note= "transmembrane domain 1"
 FT Domain 67..87
 FT /note= "transmembrane domain 2"
 XX
 XX WO9854317-A1.
 XX
 XX 03-DEC-1998.
 XX
 XX 29-MAY-1998; 98WO-EP003437.
 XX
 XX 30-MAY-1997; 97US-0048057P.
 XX
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 XX
 XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 XX WPI; 1999-059835/05.
 DR N-PSDB; AA08231.
 XX
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 PT
 XX Claim 2; Page 37; 55pp; English.
 XX
 XX This is the amino acid sequence of a CCR5 variant protein, designated
 CC CCR5m303, that comprises the first two transmembrane domains of wild-type
 CC CCR5 (see AA08231), but lacks transmembrane domains 3-7. CCR5 serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of

CC HIV-1. The presence of the CCR5m303 variant allele (see AAV84125) with
 CC the wild type CCR5 allele in an individual shows a positive correlation
 CC with resistance to infection with M-tropic HIV-1 strains, and may
 CC indicate slower progression of the disease. The detection of CCR5
 CC variants may be used to identify individuals at lower risk of infection
 CC relative to the general population who, if infected, may exhibit slower
 CC progression to AIDS. Probes and primers (see AAV84127-36) are provided
 CC for use in diagnostic methods for detecting the presence of such
 CC variants. A method is provided for inhibiting HIV-1 infection of a cell
 CC expressing the CCR5 receptor. This involves introducing a nucleic acid
 CC encoding a CCR5 variant into the cell, thereby reducing the number of
 CC functional CCR5 molecules present on the cell surface
 XX

SQ Sequence 100 AA;

Query Match 100.0%; Score 94; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 7.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
 Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 8

AAW27406
 ID AAW27406 standard; protein; 184 AA.

XX AC AAW27406;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW predisposition; resistance; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX PN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX PA (EURO-) EUROSCREEN SA.

XX PI Samson M, Parmentier M, Vassart G, Libert F;

XX DR WPI; 1997-479829/44.

XX DR N-PSDB; AAT90116.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 XX disease and viral infection.

XX PS Claim 1; Fig 1a; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
 XX 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1
 XX or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat
 XX and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
 XX glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
 XX viral infections, especially HIV-1 or HIV-2 infection, cancer,
 XX atherosclerosis and autoimmune disorders. Subjects that express the
 XX inactive receptor have a predisposition, or resistance to HIV-1 and/or

CC HIV-2
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 94; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
 Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 9

AAW27408
 ID AAW27408 standard; protein; 215 AA.

XX AC AAW27408;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW predisposition; resistance; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX PN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX PA (EURO-) EUROSCREEN SA.

XX PI Samson M, Parmentier M, Vassart G, Libert F;

XX DR WPI; 1997-479829/44.

XX DR N-PSDB; AAT90116.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 XX disease and viral infection.

XX PS Claim 7; Fig 1d-e; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
 XX 5 (CCR5), which lacks the last 3 transmembrane regions and the regions
 XX involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,
 XX treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
 XX glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
 XX viral infections, especially human immunodeficiency virus type 1 or type
 XX 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune
 XX disorders. Subjects that express the inactive receptor have a
 XX predisposition, or resistance to HIV-1 and/or HIV-2

XX SQ Sequence 215 AA;

Query Match 100.0%; Score 94; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
 Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 10

AAW88238
ID AAW88238 standard; protein; 215 AA.

XX AC AAW88238;

XX DT 15-MAR-1999 (first entry)

XX DE HIV-1 co-receptor CCR5 variant CCR5-delta32.

XX KW HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
KW gene therapy; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 32..56

XX FT /note= "transmembrane domain 1"

XX FT Domain 67..87

XX FT /note= "transmembrane domain 2"

XX FT Domain 103..124

XX FT /note= "transmembrane domain 3"

XX FT Domain 142..167

XX FT /note= "transmembrane domain 4"

XX KW W09854317-A1.

XX FN W09854317-A1.

XX PD 03-DEC-1998.

XX PF 29-MAY-1998; 98WO-EP003437.

XX PR 30-MAY-1997; 97US-0048057P.

XX PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX PI Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;

XX DR WPI; 1999-059835/05.

XX DR N-PSDB; AAW84159.

XX PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
resistance of CCR5-expressing cells to HIV-1 infection.

XX PS Disclosure; Page 38-39; 55pp; English.

XX CC This is the amino acid sequence of a CCR5 variant protein, designated
CCR5-delta32, that includes the first 4 transmembrane domains of wild-
type CCR5 (see AAW88232), but lacks transmembrane domains 5-7. CCR5
serves as a co-receptor for infection by macrophage-tropic (M-tropic)
strains of HIV-1. Individuals homozygous for the CCR5-delta32 mutation
are resistant to HIV-1 infection, but heterozygous individuals are
susceptible. The invention additionally relates to the identification of
variant CCR5s (see AAW88231), which lack transmembrane domains 3-7 of
CCR5. The detection of CCR5 variants may be used to identify individuals
at lower risk of infection relative to the general population who, if
infected, may exhibit slower progression to AIDS. Probes and primers (see
AAW84127-36) are provided for use in diagnostic methods for detecting the
presence of such variants. A method is provided for inhibiting HIV-1
infection of a cell expressing the CCR5 receptor. This involves
introducing a nucleic acid encoding a CCR5 variant into the cell, thereby
reducing the number of functional CCR5 molecules present on the cell
surface

XX SQ Sequence 215 AA;

Query Match 100.0%; Score 94; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.8e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18

|||||

Db 33 LPPLYSLVIFGFGVGNML 50

RESULT 11

AAW46859

ID AAW46859 standard; protein; 329 AA.

XX AC AAW46859;

XX DT 16-AUG-2001 (revised)

XX DT 02-AUG-2001 (revised)

XX DT 04-MAY-2001 (first entry)

XX KW Human MCP-1 receptor protein fragment.

XX DE HDGMR10; human; G-protein chemokine receptor; antiinflammatory;
KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
KW cytostatic; antiparasitic; antipneumonia; antirheumatic; antiarthritic;
KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
KW T-cell mediated autoimmune disease; psoriasis; allergy; atherosclerosis;
KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
KW hyper-eosinophilic syndrome; vulnery.

XX OS Homo sapiens.

XX FN US2001000241-A1.

XX PD 12-APR-2001.

XX PF 29-NOV-2000; 2000US-00725285.

XX PR 06-JUN-1995; 95US-00466343.

XX PR 18-NOV-1998; 98US-00195662.

XX PR 25-JUN-1999; 99US-00339912.

XX PA (LIVY/) LI Y.

XX PA (RUBE/) RUBEN S M.

XX PI Li Y, Ruben SM;

XX DR WPI; 2001-226317/23.

XX PT New human G-protein chemokine receptor polypeptides and polynucleotides,
PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX PS Disclosure; Page 16-17; 22pp; English.

XX CC This invention describes a novel receptor polypeptide (I) selected from
CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
CC products of the invention have antiinflammatory, immunomodulatory,
CC anticoagulant, antiparasitic, antirheumatic, antiallergic and vasotropic
CC activity and can be used for gene therapy. The G-protein chemokine
CC receptors, HDGMR10, (I) are useful for screening for compounds which
CC activate or inhibit activation of (I). The products of the invention can
CC also be used for stimulating haematopoiesis, wound healing, coagulation,
CC angiogenesis, treating solid tumours, chronic infections, leukemia, I-
CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
CC stimulating growth factor activity. HDGMR10 is useful for treating
CC allergy, atherosclerosis, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
CC reactions, prostaglandin-independent fever, bone marrow failure,
CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
XX errors in the keyword formatting)

SQ Sequence 329 AA;

Query Match 100.0%; Score 94; DB 4; Length 329;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
 DB 28 LPPLYSLVFIFGVGNML 45

RESULT 12
 ABB81055
 ID ABB81055 standard; protein; 329 AA.
 XX
 AC ABB81055;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human MCP-1 receptor.
 XX
 KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGMR10;
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
 KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;
 KW antirheumatic; antiarthritic; gene therapy; human; MCP-1; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002076745-A1.
 XX
 PD 20-JUN-2002.
 XX
 PF 18-NOV-1998; 98US-00195662.
 XX
 PR 06-JUN-1995; 95US-00466343.
 XX
 PA (LIYY/) LI Y.
 XX
 PA (RUBE/) RUBEN S M.
 XX
 PI Li Y, Ruben SM;
 XX
 WPI; 2002-598724/64.
 XX
 PT New polynucleotide encoding a human G protein chemokine receptor HDGMR10,
 PT useful e.g. for treating tumors.
 XX
 PS Example; Fig 2; 22pp; English.
 XX
 CC The invention relates to a novel human 7-transmembrane receptor, HDGMR10,
 CC which has been identified as a G-protein chemokine receptor. The GPCR
 CC HDGMR10 polypeptide can be expressed by standard recombinant methodology.
 CC Compounds that activate or inhibit the receptor polypeptide, optionally
 CC expressed from DNA in gene therapy vectors, are used to treat diseases
 CC that require: (a) activation of the receptor (e.g. stimulation of
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
 CC etc). The present sequence represents a human MCP-1 receptor used in
 CC comparison studies with the HDGMR10 receptor
 XX
 SQ Sequence 329 AA;

Query Match 100.0%; Score 94; DB 5; Length 329;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
 DB 28 LPPLYSLVFIFGVGNML 45

RESULT 13
 AAW26766
 ID AAW26766 standard; protein; 332 AA.
 XX

AC AAW26766;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Human chemokine receptor MMLR-CCR.
 XX
 KW Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;
 KW monocyte; macrophage; chemotaxis; haematopoiesis; infection;
 KW inflammation; proliferative disease; cardiovascular disease; tumour;
 KW rheumatoid arthritis; alveolitis; atherosclerosis;
 KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;
 KW inflammatory bowel disease; toxic shock syndrome; septic shock;
 KW Chediak-Higashi syndrome; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 107..128
 FT /note= "conserved peptide"
 FT Misc-difference 121
 FT /note= "a claimed polypeptide has isoleucine at residue
 FT 121"
 XX
 PN W09741225-A2.
 XX
 PD 06-NOV-1997.
 XX
 PF 25-APR-1997; 97WO-US006993.
 XX
 PR 26-APR-1996; 96US-00638081.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Au-Young J, Bandman O, Coleman R, Wilde CG;
 XX
 WPI; 1997-549729/50.
 DR N-PSDB; AAT99542.
 XX
 PT Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful
 PT to study, diagnose and treat, e.g. infection, inflammation, solid tumour
 PT and proliferative and cardiovascular disease.
 XX
 PS Claim 8; Page 37-38; 59pp; English.
 XX
 CC This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
 CC associated with monocyte/macrophage infiltration and chemotaxis and
 CC haematopoiesis. The amino acid sequence was deduced from a cDNA clone
 CC (see AAT99542) obtained from a cDNA library made from mononuclear cells
 CC collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
 CC with inflammation and immunomodulation. Another novel chemokine receptor,
 CC MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7
 CC transmembrane spanning segments connected by a series of intracellular
 CC and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study,
 CC diagnose and treat disease states in which normal leukocyte function is
 CC perturbed by normal leukopoiesis or inappropriate activation via
 CC chemokine agonists or antagonists, such as infection, inflammation,
 CC proliferative disease, tumorigenesis, autoimmune disease, abnormal cell
 CC proliferation, solid tumours, cardiovascular disease, rheumatoid
 CC arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
 CC asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
 CC shock syndrome, septic shock and Chediak-Higashi syndrome
 XX
 SQ Sequence 332 AA;

Query Match 100.0%; Score 94; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
 DB 24 LPPLYSLVFIFGVGNML 41

RESULT 14

ABG92881 ID ABG92881 standard; peptide; 344 AA.
 XX AC ABG92881;
 XX DT 19-NOV-2002 (first entry)
 XX DE Class I receptors WSXWS motif.
 XX KW Immunoglobulin, variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.
 XX OS Synthetic.
 XX PN WO200264612-A2.
 XX PD 22-AUG-2002.
 XX PF 08-FEB-2002; 2002WO-US003634.
 XX PR 09-FEB-2001; 2001US-00779880.
 PR 09-FEB-2001; 2001WO-US004153.
 PR 12-JUN-2001; 2001US-0297257P.
 PR 08-AUG-2001; 2001US-0310458P.
 PR 12-OCT-2001; 2001US-0328447P.
 PR 21-DEC-2001; 2001US-0341725P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Roschke V, Rosen CA, Ruben SM;
 XX DR WPI; 2002-643455/69.
 XX PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX PS Example 17; Page 386; 562pp; English.
 XX CC The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
 CC sequence of the WSXWS motif found in class I receptors
 XX SQ Sequence 344 AA;

Query Match 100.0%; Score 94; DB 5; Length 344;

Best Local Similarity 100.0%; Pred. No. 2.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIQFVGNNML 18
 DB 28 LPPLYSLVFIQFVGNNML 45

RESULT 15

ABU61655 ID ABU61655 standard; protein; 344 AA.
 XX AC ABU61655;
 XX DT 08-AUG-2003 (first entry)
 XX DE Human monocyte chemoattractant protein 1 (MCP-1) receptor.
 KW Human; G-protein chemokine receptor; receptor; HDGNR10; MCP-1;
 KW 7-transmembrane receptor; monocyte chemoattractant protein 1.
 XX OS Homo sapiens.
 XX PN US2003023044-A1.
 XX PD 30-JAN-2003.
 XX PF 03-SEP-2002; 2002US-00232686.
 XX PR 06-JUN-1995; 95US-00466343.
 PR 18-NOV-1998; 98US-00195662.
 PR 25-JUN-1999; 99US-00339912.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Li Y, Ruben SM;
 XX DR WPI; 2003-456307/43.
 XX PT Producing an antibody, involves immunizing an animal with a polypeptide
 PT or with a polypeptide encoded by the human G-protein chemokine receptor
 PT clone in ARCC 97183, and recovering the antibody.
 XX PS Disclosure; Fig 2; 23pp; English.
 XX CC The invention relates to a method of producing an antibody, involving
 CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)
 CC polypeptide (also referred to as a human 7-transmembrane receptor) and
 CC recovering an antibody which binds the polypeptide. The method is useful
 CC for producing an antibody which binds specifically to the human G-protein
 CC chemokine receptor polypeptide. This sequence represents the monocyte
 CC chemoattractant protein 1 (MCP-1) receptor which shares homology with the
 CC HDGNR10 polypeptide of the invention
 XX SQ Sequence 344 AA;

Query Match 100.0%; Score 94; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 2.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIQFVGNNML 18
 DB 28 LPPLYSLVFIQFVGNNML 45

RESULT 16

AAW27407 ID AAW27407 standard; protein; 352 AA.
 XX AC AAW27407;
 XX DT 14-APR-1998 (first entry)

XX DE Human CCR5.
 XX KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX OS Homo sapiens.
 XX FN WO9732019-A2.
 XX PD 04-SEP-1997.
 XX PF 28-FEB-1997; 97WO-BE000023.
 XX PR 01-MAR-1996; 96EP-00870021.
 XX PR 06-AUG-1996; 96EP-00870102.
 XX PA (EURO-) EUROSCREEN SA.
 XX PI Samson M, Parmentier M, Vassart G, Libert F;
 XX DR WPI; 1997-479829/44.
 XX DR N-PSDB; AAT90117.
 XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX PS Claim 4; Fig 1b-c; 94pp; English.
 XX CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
 CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 94; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIQFGVGNML 18
 DB 33 LPPLYSLVFIQFGVGNML 50
 RESULT 17
 AAW27123
 ID AAW27123 standard; protein; 352 AA.
 XX AC AAW27123;
 XX DT 14-DEC-1997 (first entry)
 XX DE Human chemokine receptor 88C.
 XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 KW modulator; antibody; human.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers

FT Domain 1..32
 FT /label= Extracellular_domain
 FT Domain 56..67
 FT /label= Intracellular_domain
 FT Domain 89..112
 FT /label= Extracellular_domain
 FT Domain 125..145
 FT /label= Intracellular_domain
 FT Domain 166..191
 FT /label= Extracellular_domain
 FT Domain 213..235
 FT /label= Intracellular_domain
 FT Domain 259..280
 FT /label= Extracellular_domain
 FT Domain 301..352
 FT /label= Intracellular_domain
 XX WO9722698-A2.
 XX 26-JUN-1997.
 XX 20-DEC-1996; 96WO-US020759.
 XX 20-DEC-1995; 95US-00575967.
 XX 07-JUN-1996; 96US-00661393.
 XX (ICOS-) ICOS CORP.
 XX Gray PW, Schweickart VL, Raport CJ;
 XX WPI; 1997-341689/31.
 XX DR N-PSDB; AAT85161.
 XX PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 PT tumours, viral infections, auto-immune diseases, etc.
 XX Claim 16; Page 47-48; 65pp; English.
 XX This polypeptide sequence comprises novel human chemokine receptor 88C, a
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
 CC macrophage library. It shows 62% identity to CCRRL1. Chemokine receptor
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
 CC and their polypeptide fragments can be produced in transformed host
 CC cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 94; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIQFGVGNML 18
 DB 33 LPPLYSLVFIQFGVGNML 50
 RESULT 18
 AAW07602
 ID AAW07602 standard; protein; 352 AA.
 XX AC AAW07602;
 XX DT 26-FEB-1997 (first entry)
 XX DE Human G-protein chemokine receptor HDGNR10.

```

XX G-protein chemokine receptor; HDGMR10; signal transduction;
KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
XX WO9639437-A1.
XX
XX 12-DEC-1996.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 1997-043072/04.
XX
XX N-PSDB; AAT44042.
XX
XX Human G-protein chemokine receptor, HDGMR10 - useful to identify
XX (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
XX acute inflammation, rheumatoid arthritis, etc.
XX
XX Claim 1; Page 44-46; 61pp; English.
XX
XX Novel human mature G-protein chemokine receptor HDGMR10 (AAW07602) is a 7
XX -transmembrane protein involved in signal transduction. Its amino acid
XX sequence was deduced from a cDNA clone (AAT44042) isolated from a human
XX monocyte library. Isolation of the cDNA allows prodn. of recombinant
XX HDGMR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
XX receptor can be used to identify agonists or antagonists of the receptor;
XX such cpds. can be used to treat conditions related to the under- and over
XX -expression of G-protein chemokine receptors
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 94; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 3e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LPPLYSLVFIQFGVGNML 18
XX Db 33 LPPLYSLVFIQFGVGNML 50
XX
XX RESULT 19
XX ID AAW23835
XX AC AAW23835 standard; protein; 352 AA.
XX
XX AC AAW23835;
XX
XX DT 08-JUN-1998 (first entry)
XX
XX Human CC chemokine receptor 5 (CCR5).
XX
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
XX human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Domain 29..55
XX FT /label= I
XX FT /note= "transmembrane domain"
XX FT 104..126
XX FT /label= III
XX FT /note= "transmembrane domain"
XX FT 109..120
XX FT Region
XX FT /note= "extracellular loop-1 (Claim 19)"
XX FT 143..171

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FT /label= IV
FT /note= "transmembrane domain"
FT 187..210
FT /note= "extracellular loop-2 (Claim 19)"
FT 194..219
FT /label= V
FT /note= "transmembrane domain"
FT 238..258
FT /label= VI
FT /note= "transmembrane domain"
FT 261..276
FT /note= "extracellular loop-3 (Claim 19)"
FT 277..300
FT /label= VII
FT /note= "transmembrane domain"
XX
XX WO9745543-A2.
XX
XX 04-DEC-1997.
XX
XX 28-MAY-1997; 97WO-US009586.
XX
XX 28-MAY-1996; 96US-0018508P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Combadriere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
XX Broder CC, Kennedy PE;
XX WPI; 1998-032650/03.
XX N-PSDB; AAT76920.
XX
XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
XX between HIV and a target cell.
XX
XX Claim 68; Fig 1C; 70pp; English.
XX
XX This protein sequence comprises of a novel human macrophage-selective CC
XX chemokine receptor that has been designated CCR5. The sequence was
XX deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant
XX (see W238340 of CCR5 was also identified. The susceptibility of human
XX macrophages to HIV infection depends on cell surface expression of CD4
XX and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
XX protein coupled cell surface molecules. It plays an essential role in the
XX membrane fusion step of infection by some HIV isolates. The establishment
XX of stable, non-human cell lines and transgenic mammals having cells that
XX coexpress human CD4 and CCR5 provides valuable tools for research of HIV
XX infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX agents capable of blocking membrane fusion between HIV and target cells
XX represent potential anti-HIV therapeutics for macrophage tropic strains
XX of HIV
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 94; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 3e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LPPLYSLVFIQFGVGNML 18
XX Db 33 LPPLYSLVFIQFGVGNML 50
XX
XX RESULT 20
XX ID AAW88232
XX AC AAW88232 standard; protein; 352 AA.
XX
XX AC AAW88232;
XX
XX 15-MAR-1999 (first entry)
XX
XX HIV-1 co-receptor CCR5.
XX

```


KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
KW gene therapy; human.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Domain 32..56

FT Domain /note= "transmembrane domain 1"

FT Domain 67..87

FT Domain /note= "transmembrane domain 2"

FT Misc-difference 101

FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA

FT (Stop) in CCR5m303"

FT Domain 103..124

FT Domain /note= "transmembrane domain 3"

FT Domain 142..167

FT Domain /note= "transmembrane domain 4"

FT Domain 200..223

FT Domain /note= "transmembrane domain 5"

FT Domain 236..260

FT Domain /note= "transmembrane domain 6"

FT Domain 275..301

FT Domain /note= "transmembrane domain 7"

XX WO9854317-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-EP003437.

XX 30-MAY-1997; 97US-0048057P.

XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX Beretta A, Quillent C, Arenzana Siededors F, Braun J;

XX WPI; 1999-059835/05.

XX N-PSDB; AAV84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
XX resistance of CCR5-expressing cells to HIV-1 infection.

XX Disclosure; Page 34-35; 55pp; English.

XX This is the amino acid sequence of wild-type human CCR5, which serves as
XX a co-receptor for infection by macrophage-tropic (M-tropic) strains of
XX HIV-1. The invention relates to the identification of a CCR5 variant (see
XX AAV84127), designated CCR5m303, comprising the first two transmembrane
XX domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
XX presence of the CCR5m303 variant with the wild type CCR5 allele shows a
XX positive correlation with resistance to infection with M-tropic HIV-1
XX strains, and may indicate slower progression of the disease. The
XX detection of CCR5 variants may be used to identify individuals at lower
XX risk of infection relative to the general population who, if infected,
XX may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
XX 36) are provided for use in diagnostic methods for detecting the presence
XX of such variants. A method is provided for inhibiting HIV-1 infection of
XX a cell expressing the CCR5 receptor. This involves introducing a nucleic
XX acid encoding a CCR5 variant into the cell, thereby reducing the number
XX of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LPPLYSLVFIQFGVGNML 18

|||||

Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 21

AAV80128

ID AAV80128 standard; protein; 352 AA.

XX AC AAV80128;

XX 19-MAY-2000 (first entry)

XX Human G-protein chemokine receptor HDGMR10 SEQ ID NO:2.

XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGMR10;
XX diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
XX tumour; infection; leukaemia; psoriasis; allergy;
XX T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
XX inflammation; allergic reaction; silicosis; sarcoidosis;
XX rheumatoid arthritis; hyper-eosinophilia syndrome.

XX Homo sapiens.

XX US6025154-A.

XX 15-FEB-2000.

XX 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI; 2000-181807/16.

XX N-PSDB; AAZ91481.

XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
XX for diagnostic assays, scientific research and screening for compounds
XX which bind to and activate or inhibit activation of the receptor
XX polypeptides.

XX Claim 1; Fig 1; 22pp; English.

XX The present sequence represents a human G-protein chemokine receptor
XX designated HDGMR10. HDGMR10 polynucleotides are useful in methods of
XX screening for compounds which bind to and either: (1) activate the
XX HDGMR10 polypeptides causing stimulation of haematopoiesis, wound
XX healing, coagulation, and angiogenesis; treatment of solid tumours,
XX chronic infections, leukaemia, T-cell mediated autoimmune diseases,
XX parasitic infections, psoriasis, and to stimulate growth factor activity;
XX or (2) inhibit activation of the HDGMR10 polypeptides which is useful for
XX preventing and/or treating allergy, atherogenesis, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and immunoglobulin
XX E-mediated allergic reactions, prostaglandin-independent fever, bone
XX marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
XX hyper-eosinophilia syndrome. The polynucleotides are also useful for
XX diagnostic assays for detecting diseases related to mutations in the
XX nucleic acid sequences encoding the polypeptides and for detecting an
XX altered level of the soluble form of the receptor polypeptides. The
XX polynucleotides are also useful for in vitro purposes related to
XX scientific research, synthesis of DNA and manufacture of DNA vectors

XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LPPLYSLVFIQFGVGNML 18

|||||

Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 22

AAV79089

ID AAV79089 standard; protein; 352 AA.

CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGNR10 protein
 XX
 XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFVGNML 18
 DB 33 LPPLYSLVIFGFVGNML 50

RESULT 24
 ID AAE07048 standard; protein; 352 AA.

AAE07048;
 16-OCT-2001 (first entry)

Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 cardiovascular disorder; myocardial ischaemia.

Homo sapiens.

WO200158916-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US0004153.

09-FEB-2000; 2000US-0181258P.

09-MAR-2000; 2000US-0187999P.

22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Roschke V, Li Y, Ruben SM;

WFI; 2001-488966/53.

N-PSDB; AADI3299.

PT Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

CC The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGNR10 protein
 XX
 XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
 DB 33 LPPLYSLVIFGFVGNML 50

RESULT 25

AAAG80111
 ID AAG80111 standard; protein; 352 AA.

AC AAG80111;

DT 17-JAN-2002 (first entry)

DE Human CCR5 protein.

Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 antirheumatic; antiarthritic.

Homo sapiens.

WO200172830-A2.

04-OCT-2001.

02-APR-2001; 2001WO-EP003708.

31-MAR-2000; 2000DE-01016013.

(IPFP-) IPF PHARM GMBH.

(FORS/) FORSSMANN U.

Forssmann W, Adermann K, Heitland A, Spodberg N;

DR WP1; 2001-626256/72.
 XX
 PT Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX
 PS Disclosure; Page 10; 26pp; German.
 XX
 CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antirheumatic, antiarthritic,
 CC immunosuppressive, dermatological, antitumor, antiproliferative, and
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG8004S-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFVGNML 18
 DB 33 LPPLYSLVIFGFVGNML 50
 RESULT 26
 AAE04321
 ID AAE04321 standard; protein; 352 AA.
 XX
 AC AAE04321;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human chemokine receptor (CCR), CC-CR5-5 related protein #2.
 KW Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CR5; envelope glycoprotein; anti-HIV.
 XX
 OS Homo sapiens.
 XX
 PN US6258527-B1.
 XX
 PD 10-JUL-2001.
 XX
 PF 21-MAY-1997; 97US-00861105.
 XX
 PR 20-MAY-1996; 96US-0017157P.
 PR 19-JUN-1996; 96US-0020043P.
 PR 19-MAY-1997; 97US-00858660.
 XX
 PA (AARO-) AARON DIAMOND AIDS RES CENT.
 PA (UUNY) UNIV NEW YORK STATE.
 XX
 PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;
 XX
 XX WP1; 2001-417127/44.
 DR N-P8DB; AAD08577.
 DR
 XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of

PT HIV.
 XX
 PS Disclosure; Col 47-50; 37pp; English.
 XX
 CC The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CR5-5 related protein.
 CC CC-CR5 is the principal cofactor for entry mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFVGNML 18
 DB 33 LPPLYSLVIFGFVGNML 50
 RESULT 27
 AAE07037
 ID AAE07037 standard; protein; 352 AA.
 XX
 AC AAE07037;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 KW cytostatic; immunosuppressive; neotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 FT Domain 1..36
 FT /label= Extracellular_domain
 FT Domain 37..305
 FT /label= Transmembrane_domain
 FT Domain 37..58
 FT /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT Domain 59..67
 FT /label= Intracellular_loop_1
 FT Domain 68..88
 FT /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT Domain 89..102
 FT /label= Extracellular_loop_1
 FT Domain 103..124
 FT /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT Domain 125..141
 FT /label= Intracellular_loop_2
 FT Domain 142..166

FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT 167..195
 FT Domain
 FT /label= Extracellular_loop_2
 FT 196..223
 FT Domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT 224..235
 FT Domain
 FT /label= Intracellular_loop_3
 FT 236..260
 FT Domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT 261..274
 FT Domain
 FT /label= Extracellular_loop_3
 FT 287..305
 FT Domain
 FT /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT 306..352
 FT /label= Intracellular_domain
 FT
 PN WO200158915-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004152.
 XX 09-FEB-2000; 2000US-0181258P.
 XX 09-MAR-2000; 2000US-0187999P.
 XX 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-488965/53.
 XX N-PSDB; AAD13181.
 XX
 PT Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX
 PS Claim 102; Fig 1; 495pp; English.
 XX
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10
 CC protein. CCR5 HDGMR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 CC HDGMR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGMR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGMR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGMR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound
 CC healing
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVFIKFGVGNML 18
 |||||
 DB 33 LPPLSLVFIKFGVGNML 50
 |||||
 RESULT 28
 AAE07039
 ID AAE07039 standard; protein; 352 AA.
 XX
 AC AAE07039;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytotatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200158915-A2.
 XX
 XD 16-AUG-2001.
 XX
 PD 09-FEB-2001; 2001WO-US004152.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX
 DR WPI; 2001-488965/53.
 DR N-PSDB; AAD13198.
 XX
 PT Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX
 PS Example 40; Page 486-487; 495pp; English.
 XX
 CC The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10
 CC protein. CCR5 HDGMR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation,
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 CC a neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGMR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGMR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGMR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular

CC disorders (myocardial ischaemias) and wound healing
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFGVGNML 18
 |||||
 Db 33 LPPLYSLVIFGFGVGNML 50
 RESULT 29
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX
 AC AAB46858;
 XX
 DT 16-AUG-2001 (revised)
 DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 XX
 DE Human HDGMR10 protein.
 XX
 KW HDGMR10; human; G-protein chemokine receptor; antiinflammatory;
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
 KW cytosstatic; antiparasitic; antipsoiatric; antirheumatic; antiarthritic;
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
 KW hyper-eosinophilic syndrome; vulnery.
 KW
 XX Homo sapiens.
 OS
 XX US2001000241-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 29-NOV-2000; 2000US-00725285.
 XX
 PR 06-JUN-1995; 95US-00456343.
 PR 18-NOV-1998; 98US-00195662.
 PR 25-JUN-1999; 99US-00339912.
 XX
 PA (LIYY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Li Y, Ruben SM;
 XX
 DR WPI: 2001-226317/23.
 DR N-PSDB; AAF26390.
 XX
 PT New human G-protein chemokine receptor polypeptides and polynucleotides,
 PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
 XX
 PS Claim 1a; Page 15; 22pp; English.
 XX
 CC This invention describes a novel receptor polypeptide (I) selected from
 CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
 CC products of the invention have antiinflammatory, immunomodulatory,
 CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytosstatic,
 CC antiparasitic, antipsoiatric, antirheumatic, antiarthritic and vasotropic
 CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors, HDGMR10, (I) are useful for screening for compounds which
 CC activate or inhibit activation of (I). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-

CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 CC stimulating growth factor activity. HDGMR10 is useful for treating
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFGVGNML 18
 |||||
 Db 33 LPPLYSLVIFGFGVGNML 50
 RESULT 30
 ABB56342
 ID ABB56342 standard; protein; 352 AA.
 XX
 AC ABB56342;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Non-endogenous human GPCR protein, SEQ ID NO: 477.
 XX
 KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W0200177172-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 05-APR-2001; 2001WO-US011098.
 XX
 PR 07-APR-2000; 2000US-0195747P.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 PI Lehmann-Bruinsma K, Liaw CW, Lin I;
 XX
 DR WPI: 2001-648759/74.
 DR N-PSDB; ABI97978.
 XX
 PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.
 XX
 PS Claim 1; Page 277-278; 394pp; English.
 XX
 CC The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFGVGNML 18
 |||||

Db 33 LPPLYSLVFIQFVGNNL 50

Search completed: March 4, 2004, 17:59:20
Job time : 45.7959 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 9.18367 Seconds
(without alignments)
188.535 Million cell updates/sec

Title: US-10-084-813-11

Perfect score: 94

Sequence: 1 LPPLYSILVIFGFVGNML 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96151526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR_78.*

1: piri:*

2: piri2:*

3: piri3:*

4: piri4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	352	2	chemokine (C-C) re
2	94	100.0	360	2	chemokine (C-C) re
3	94	100.0	374	2	chemokine (C-C) re
4	77	81.9	355	2	chemokine (C-C) re
5	77	81.9	355	2	chemokine (C-C) re
6	77	81.9	359	2	macrophage inflam
7	75	79.8	360	2	MIP-1 alpha recept
8	66	70.2	360	2	chemokine (C-C) re
9	63	67.0	355	2	chemokine (C-C) re
10	62	66.0	383	2	chemokine (C-C) re
11	60	63.8	356	2	G protein-coupled
12	60	63.8	361	2	G protein-coupled
13	59	62.8	373	2	G protein-coupled
14	59	62.8	373	2	G protein-coupled
15	58	61.7	354	2	G protein-coupled
16	57	60.6	352	2	probable G protein
17	57	60.6	352	2	fusin (FUS1A) - c
18	57	60.6	362	2	neuropeptide Y/pep
19	57	60.6	367	2	G protein-coupled
20	56	59.6	316	2	interferon-inducib
21	56	59.6	327	2	hypothetical prote
22	56	59.6	333	2	MDCK15 protein - h
23	56	59.6	359	2	neuropeptide Y/pep
24	56	59.6	359	2	angiotensin II rec
25	56	59.6	359	2	angiotensin II rec
26	56	59.6	359	2	angiotensin II rec
27	56	59.6	359	2	angiotensin II rec
28	56	59.6	359	2	angiotensin II rec
29	56	59.6	359	2	angiotensin II rec

angiotensin II rec
angiotensin II rec
G protein-coupled
G protein-coupled
G protein-coupled
G protein-coupled
angiotensin II rec
angiotensin II rec
HHRF3 protein - hu
G protein-coupled
G protein-coupled
hypothetical prote
neurotensin recept
conserved hypothet
kappa opioid recep
kappa opioid recep
kappa opioid recep
kappa opioid recep
galanin receptor 2
penicillin-binding
peptidoglycan glyc
angiotensin recept
orphan G protein-c
bombesin/gastrin-r
bombesin/ GRP rece
hypothetical prote
sulfinilkin recepto
G protein-coupled
angiotensin II rec
angiotensin II rec
60 kd inner-membra
60K inner-membra
hypothetical prote
NADH2 dehydrogenas
hypothetical prote
probable holocyto
G protein-coupled
platelet activatin
thrombin receptor
gastric CCK-A rece
cholecystokinin ty
cholecystokinin A
B-alpha pheromone
G protein-coupled
platelet-activatin
G protein-coupled
gastrin-releasing
bombesin receptor,
hypothetical prote
hypothetical prote
hypophan-specifi
hypothetical prote
H+transporting tw
high-affinity bran
hypothetical prote
hypothetical prote
transporter yxfa l
complement C5a ana
G protein-coupled
delta opioid recep
G protein-coupled
lymphocyte-specifi
cholecystokinin re
prostaglandin E2 r

30 56 59.6 359 2 JH0621
31 56 59.6 359 2 JC2134
32 56 59.6 372 2 S26667
33 56 59.6 374 2 S42628
34 56 59.6 374 2 S32785
35 56 59.6 387 2 I69202
36 54 57.4 359 2 JQ1516
37 54 57.4 359 2 I51372
38 53 56.4 323 1 Q08ED3
39 53 56.4 359 2 T09353
40 53 56.4 369 2 JC5068
41 52 55.3 326 2 T25301
42 52 55.3 416 2 S68822
43 50 53.2 175 2 C69398
44 50 53.2 380 2 JC2434
45 50 53.2 380 2 A48227
46 50 53.2 380 2 JC2338
47 50 53.2 380 2 S36143
48 50 53.2 380 2 A55259
49 50 53.2 387 2 JC5949
50 50 53.2 821 2 E95245
51 50 53.2 821 2 B93110
52 49 52.1 380 2 I38435
53 48 51.1 355 2 JC4304
54 48 51.1 384 2 A39003
55 48 51.1 384 2 I57682
56 48 51.1 425 2 T15959
57 48 51.1 584 2 JC7809
58 47 50.0 360 2 G02064
59 47 50.0 363 2 I48261
60 47 50.0 363 2 A49092
61 47 50.0 363 2 JC2543
62 47 50.0 370 1 I52315
63 46.5 49.5 376 2 T24368
64 46 48.9 362 2 JN0694
65 46 48.9 560 2 H71712
66 46 48.9 560 2 B97709
67 45.5 48.4 472 2 F90078
68 45 47.9 174 2 T11400
69 45 47.9 177 2 D72512
70 45 47.9 213 2 E64030
71 45 47.9 333 2 I65989
72 45 47.9 341 2 S63666
73 45 47.9 342 2 S13638
74 45 47.9 420 2 I51667
75 45 47.9 427 2 S50150
76 45 47.9 428 2 JN0692
77 45 47.9 430 2 I51898
78 44 46.8 323 2 S61919
79 44 46.8 328 2 I55450
80 44 46.8 341 2 S43252
81 44 46.8 342 2 A40191
82 44 46.8 350 2 JN0621
83 44 46.8 384 2 A41007
84 44 46.8 390 2 B41007
85 44 46.8 444 2 T27866
86 44 46.8 455 2 T15622
87 43.5 46.3 411 2 A82492
88 43 45.7 178 2 A64399
89 43 45.7 241 2 S01147
90 43 45.7 295 2 A03552
91 43 45.7 295 2 A03063
92 43 45.7 295 2 H98222
93 43 45.7 295 2 H86907
94 43 45.7 351 1 A46525
95 43 45.7 355 2 JC5067
96 43 45.7 373 2 J80087
97 43 45.7 378 2 A45680
98 43 45.7 378 2 B55735
99 43 45.7 444 2 A42685
100 43 45.7 488 2 A53572

chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
C:Accession: A43113; S71808; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A>Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A:Accession number: A43113; MUID:96241590; PMID:8639485
A:Reference: A3113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:g1262810; PIDN:CAAG2796.1; PID:g1262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Llesnard, C.; Barber, C.M.; Sargost
M.; Inai, T.; Rana, S.; Yi, Y.; Smyth, R.G.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa
Nature 382, 722-725, 1996
A>Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A:Accession number: S71808; MUID:96345670; PMID:8751444
A:Reference: A31808
A:A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206;207-230 <SAM2>
A:Accession: A58833
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184; 'IKDSHLGAGPAAACHGHLILGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X99393; NID:g1524062; PIDN:CAAG7767.1; PID:g1524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
R:Combadieere, C.; Anujya, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A>Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadieere, C.
submitted to the EMBL Data Library, May 1996
A:Accession: H01541
A:Reference: G02653
A:Status: translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-89, 'L', '91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Rapport, C.J.; Goelling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A>Title: Molecular cloning and functional characterization of a novel human CC chemokine
A:Reference number: A58833; MUID:96291862; PMID:8663314
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:g1457945; PIDN:AACS0598.1; PID:g1457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see
C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine
C:Genetics.
A:Gene: GB:CKR5; CCR5; CKR-5; CC-CKR-5; CCR5; ChemR13
A:Cross-references: GDB:I230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A:Note: Probably acts to control granulocyte proliferation and differentiation
C:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F:32-56/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>

C:Accession: I38450
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U03882; NID:g472555; PIDN:AAAL9119.1; PID:g472556
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F:44-68/Domain: transmembrane #status predicted <TM>
F:79-99/Domain: transmembrane #status predicted <TM>
F:115-136/Domain: transmembrane #status predicted <TM>
F:154-178/Domain: transmembrane #status predicted <TM>
F:208-226/Domain: transmembrane #status predicted <TM>
F:244-265/Domain: transmembrane #status predicted <TM>
F:292-309/Domain: transmembrane #status predicted <TM>
F:32-277/Domain: transmembrane #status predicted <TM>
F:13/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 100.0%; Score 94; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
Db 45 LPPLYSLVVFIFGVGNML 62

RESULT 4
A45177
chemokine (C-C) receptor 1 - human
N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: A45177; I55671
R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor
A:Reference number: A45177; MUID:93161416; PMID:7679328
A:Accession: A45177
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-355 <NEO>
A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A:Experimental source: HL60 cells
A:Note: sequence extracted from NCBI backbone (NCBI:124876)
R:Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A:Title: Structure and functional expression of the human macrophage inflammatory protein 1 alpha
A:Reference number: I55671; MUID:93240122; PMID:7683036
A:Accession: I55671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>
A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C:Genetics:
A:Gene: GDB:CMKBR1; CMKR-1
A:Cross-references: GDB:138446; OMIM:601159
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:36-60/Domain: transmembrane #status predicted <TM>
F:71-91/Domain: transmembrane #status predicted <TM>
F:108-129/Domain: transmembrane #status predicted <TM>
F:147-171/Domain: transmembrane #status predicted <TM>
F:205-223/Domain: transmembrane #status predicted <TM>

F:240-264/Domain: transmembrane #status predicted <TM>
F:288-305/Domain: transmembrane #status predicted <TM>
F:3/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:24-273,106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 81.9%; Score 77; DB 2; Length 355;
Best Local Similarity 77.8%; Pred. No. 6.4e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
Db 37 LPPLYSLVVFIFGVGNML 54

RESULT 5
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49339
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C:Superfamily: vertebrate rhodopsin

Query Match 81.9%; Score 77; DB 2; Length 355;
Best Local Similarity 83.3%; Pred. No. 6.4e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
Db 37 LPPLYSLVVFIFGVGNML 54

RESULT 6
I49341
MIP-1 alpha receptor like-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
C:Accession: I49341
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U28406; NID:g881551; PID:g881552
C:Superfamily: vertebrate rhodopsin

Query Match 81.9%; Score 77; DB 2; Length 359;
Best Local Similarity 77.8%; Pred. No. 6.4e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
Db 41 LPPLYSLVVFIFGVGNML 58

RESULT 7
A57160
chemokine (C-C) receptor 4 - human
N:Alternate names: C-C CKR-4
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

C;Accession: A57160
 R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; J. Biol. Chem. 270, 19498-19500, 1995
 A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor c
 C;Date: 21-Dec-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 A;Reference number: A57160; MUID:95370289; PMID:7642634
 A;Accession: A57160
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-360 <POW>
 A;Cross-references: GB:X85740; NID:gl370103; PIDN:CAA59743.1; PID:g971452
 A;Note: source clone X5-5
 C;Genetics:
 A;Gene: GDB:CMKBR4
 A;Cross-references: GDB:677463
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F;40-65/Domain: transmembrane #status predicted <TM1>
 F;76-97/Domain: transmembrane #status predicted <TM2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;243-264/Domain: transmembrane #status predicted <TM6>
 F;291-308/Domain: transmembrane #status predicted <TM7>
 F;29-276,110-187/Disulfide bonds: #status predicted
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;183,194/Binding site: carbonylate (Asn) (covalent) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 Query Match 79.8%; Score 75; DB 2; Length 360;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIQFGVGN 16
 DB 42 LPPLSLVFIQFGVGN 57
 |||||:|:|:|
 |||||:|:|:|
 RESULT 8
 JC4587
 chemokine (C-C) receptor 4 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C;Accession: JC4587
 R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A. Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A;Reference number: JC4587; MUID:96136324; PMID:8573157
 A;Accession: JC4587
 A;Molecule type: mRNA
 A;Residues: 1-360 <HO>
 A;Cross-references: EMBL:X90862; NID:gl167851; PIDN:CAA62372.1; PID:gl167852
 A;Experimental source: thymus
 C;Genetics:
 A;Gene: cc ckr-4
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F;2,183,194/Binding site: carbonylate (Asn) (covalent) #status predicted
 F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 Query Match 70.2%; Score 66; DB 2; Length 360;
 Best Local Similarity 75.0%; Pred. No. 0.0041;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIQFGVGN 16
 DB 42 LPPLSLVFIQFGVGN 57
 |||||:|:|:|
 |||||:|:|:|
 RESULT 9
 JC4587
 chemokine (C-C) receptor 3 - human
 N;Alternate names: C-C CKR-3
 C;Species: Homo sapiens (man)
 C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
 C;Accession: G02436; A57237
 R;Ponath, P.D. submitted to the EMBL Data Library, February 1996
 A;Reference number: H01272
 A;Accession: G02436
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <PON>
 A;Cross-references: EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477561
 R;Comadriere, C.; Abuja, S.K.; Murphy, P.M. J. Biol. Chem. 270, 16491-16494, 1995
 A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
 A;Reference number: A57237; MUID:95348056; PMID:7622448
 A;Accession: A57237
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
 A;Cross-references: GB:U28694; NID:gl199579; PIDN:AAC50469.1; PID:gl199580
 A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
 C;Genetics:
 A;Gene: GDB:CMKBR3
 A;Cross-references: GDB:579624; OMIM:601268
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-261/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 Query Match 67.0%; Score 63; DB 2; Length 355;
 Best Local Similarity 61.1%; Pred. No. 0.012;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIQFGVGNML 18
 DB 37 VPPLSLVFIQFGVGNV 54
 |||||:|:|:|
 |||||:|:|:|
 RESULT 10
 S55594
 G protein-coupled receptor E1 - equine herpesvirus 2
 C;Species: equine herpesvirus 2
 C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C;Accession: S55594
 R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J. J. Mol. Biol. 249, 520-528, 1995
 A;Title: The DNA sequence of equine herpesvirus 2.
 A;Reference number: S55594; MUID:95302501; PMID:7783207
 A;Accession: S55594
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-383 <TEL>
 A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor
 Query Match 66.0%; Score 62; DB 2; Length 383;
 Best Local Similarity 61.1%; Pred. No. 0.02;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIQFGVGNML 18
 |||||:|:|:|
 |||||:|:|:|

Db 75 VPALYLIVFLFGLGNIL 92

RESULT 11

I49340

C:Keywords: ATP receptor like-1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999

C:Accession: I49340

R:Geo, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptors

A:Reference number: I49339; MUID:95340546; PMID:7542241

A:Accession: I49340

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-356 <R>

A:Cross-references: EMBL:U28405; NID:9881549; PIDN:AAA89154.1; PID:g881550

C:Superfamily: vertebrate rhodopsin

Query Match 63.8%; Score 60; DB 2; Length 356;

Best Local Similarity 68.8%; Pred. No. 0.039;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PLYSLVFIQFGVGNML 18

Db 40 PLYSLVFIQFGVGNML 55

RESULT 12

B45680

C:Keywords: protein-coupled peptide receptor EBI 2 - human

C:Species: Homo sapiens (man)

C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C:Accession: B45680

R:Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled protein

A:Reference number: A45680; MUID:93188173; PMID:8383238

A:Accession: B45680

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-361 <BIR>

A:Cross-references: GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057

A:Experimental source: B-lymphocytes

A>Note: sequence extracted from NCBI backbone (NCBI:127096, NCBI:127097)

C:Superfamily: ATP receptor p2u

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 63.8%; Score 60; DB 2; Length 361;

Best Local Similarity 66.7%; Pred. No. 0.039;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18

Db 34 MPLYSLVFIQFGVGNML 51

RESULT 13

JC4162

P2Y receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999

C:Accession: JC4162

R:Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainy, I.A.

Biochem. Biophys. Res. Commun. 212, 648-656, 1995

A:Title: Cloning and characterization of a bovine P2Y receptor.

A:Reference number: JC4162; MUID:95352058; PMID:7626079

A:Accession: JC4162

A:Molecule type: mRNA

A:Residues: 1-373 <HEN>

A:Cross-references: EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g1032485

A:Experimental source: aortic endothelial cell

C:Genetics:

A:Gene: borp2y

C:Superfamily: ATP receptor P2u

C:Keywords: Glycoprotein; phosphoprotein; receptor; transmembrane protein

F:52-77/Domain: transmembrane #status predicted <TM1>

F:88-111/Domain: transmembrane #status predicted <TM2>

F:124-150/Domain: transmembrane #status predicted <TM3>

F:171-191/Domain: transmembrane #status predicted <TM4>

F:214-237/Domain: transmembrane #status predicted <TM5>

F:261-282/Domain: transmembrane #status predicted <TM6>

F:305-328/Domain: transmembrane #status predicted <TM7>

F:11.27.113.197/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 62.8%; Score 59; DB 2; Length 373;

Best Local Similarity 68.8%; Pred. No. 0.059;

Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGN 16

Db 54 LPAVILVFIQFGVGN 69

RESULT 14

JC4737

G protein-coupled receptor P2Y1 - human

N:Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C:Accession: JC4737; JC4615; S54253

R:Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A:Title: Cloning and tissue distribution of the human P2Y1 receptor.

A:Reference number: JC4737; MUID:96205320; PMID:8630005

A:Accession: JC4737

A:Molecule type: DNA

A:Residues: 1-373 <JAN>

A:Cross-references: GB:S81950; NID:g1839438; PIDN:AAA47091.1; PID:g1839439

R:Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Achwal, R.S.; Barnard, E.A.; Kunapuli, S.P.

Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A:Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A:Reference number: JC4615; MUID:96158962; PMID:8579591

A:Accession: JC4615

A:Molecule type: mRNA

A:Residues: 1-373 <AY>

A:Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731

A:Experimental source: erythro leukemia cells

R:Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.

submitted to the EMBL Data Library, May 1995

A:Description: Cloning of a human putative P2Y receptor.

A:Reference number: S54253

A:Accession: S54253

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-137,139-373 <LEO>

A:Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836

C:Comment: This receptor belongs to a family of G protein-coupled receptors. It responds

C:Genetics:

A:Gene: P2Y1; GDB:P2RY1

A:Cross-references: GDB:677125; OMIM:601167

A:Map position: 3pter-3qter

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:52-77/Domain: transmembrane #status predicted <TM1>

F:88-111/Domain: transmembrane #status predicted <TM2>

F:124-152/Domain: transmembrane #status predicted <TM3>

F:171-191/Domain: transmembrane #status predicted <TM4>

F:214-237/Domain: transmembrane #status predicted <TM5>

F:261-282/Domain: transmembrane #status predicted <TM6>

F:305-328/Domain: transmembrane #status predicted <TM7>

F:11.27.113.197/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:258/336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict

F:330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict

A45747
neuropeptide Y/pptide YY receptor Y3 - human
N:Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; re
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C:Accession: A45747; A53103; I53006; I59444; I69203; S32761
R:Pedersenpiel, B.; Mellado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewis
Genomics 16, 707-712, 1993
A:Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu

Query Match 60.6%; Score 57; DB 2; Length 362;
 Best Local Similarity 68.8%; Pred. No. 0.12;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNL 16
 ||:|||||:|:|
 Db 43 LPTVYILVITGLN 58

RESULT 19
 JE0349
 interferon-inducible protein 10 (IP-10) receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
 C:Accession: JE0349
 R:Tamari, M.; Tomimaga, Y.; Yatsunami, K.; Narumi, S.
 Biochem. Biophys. Res. Commun. 251, 41-48, 1998
 A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
 A:Reference number: JE0349; MUID:99009219; PMID:9790904
 A:Accession: JE0349
 A:Molecule type: mRNA
 A:Residues: 1-167 <TAM>
 A:Cross-references: DDBJ:AB031174; NID:93798731; PIDN:BA34045.1; PID:93798732
 C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
 C:Superfamily: vertebrate rhodopsin

Query Match 60.6%; Score 57; DB 2; Length 367;
 Best Local Similarity 62.5%; Pred. No. 0.12;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNL 16
 ||:|||||:|:|
 Db 55 LPALYSLLFLLGLGN 70

RESULT 20
 T23640
 hypothetical protein M01B2.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T23640
 R:Lloyd, C.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19776
 A:Accession: T23640
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-316 <WIL>
 A:Cross-references: EMBL:Z83116; PIDN:CAB05565.1; GSPDB:GN00023; CESP:M01B2.7
 A:Experimental source: clone M01B2
 C:Gene: CESP:M01B2.7
 A:Map position: 5
 A:Introns: 34/2, 72/1; 108/2; 160/2; 205/1; 272/2

Query Match 59.6%; Score 56; DB 2; Length 316;
 Best Local Similarity 66.7%; Pred. No. 0.15;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LYSLVIFFGVGNL 18
 ||:|||||:|:|
 Db 11 LYSTIFVGTGNL 25

RESULT 21
 S56162
 MCKR15 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
 C:Accession: S56162
 R:Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
 Biochem. J. 309, 773-779, 1995

A:Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati
 A:Reference number: S56162; MUID:95366951; PMID:7639692
 A:Accession: S56162
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-327 <BAR>
 A:Cross-references: EMBL:X68829; NID:9840783; PIDN:CAA48723.1; PID:9840784
 C:Superfamily: vertebrate rhodopsin

Query Match 59.6%; Score 56; DB 2; Length 327;
 Best Local Similarity 50.0%; Pred. No. 0.16;
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNL 18
 ||:|||||:|:|
 Db 9 VFWYSLIFLLGVGNL 26

RESULT 22
 S28787
 neuropeptide Y/peptide YY receptor Y3 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
 C:Accession: S28787
 R:Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
 Mol. Pharmacol. 40, 869-875, 1991
 A:Title: Sequence and expression of a neuropeptide Y receptor cDNA.
 A:Reference number: S28787; MUID:92100053; PMID:1661837
 A:Accession: S28787
 A:Molecule type: mRNA
 A:Residues: 1-353 <RIM>
 A:Cross-references: EMBL:M86739
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 59.6%; Score 56; DB 2; Length 353;
 Best Local Similarity 55.6%; Pred. No. 0.17;
 Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNL 18
 ||:|||||:|:|
 Db 42 LPTVYSILFVTGIVGNL 59

RESULT 23
 JC1104
 angiotensin II receptor type 1 - human
 N:Alternate names: angiotensin II receptor 1A
 C:Species: Homo sapiens (man)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000
 C:Accession: JC1104; JQ1402; JH0574; JH0267; A44014; S18983
 R:Maury, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.
 Biochem. Biophys. Res. Commun. 186, 277-284, 1992
 A:Title: Cloning, expression, and characterization of a gene encoding the human angioten
 A:Reference number: JC1104; MUID:92337608; PMID:1378723
 A:Accession: JC1104
 A:Molecule type: DNA
 A:Residues: 1-359 <MAU>
 R:Furuta, H.; Guo, D.F.; Inagami, T.
 Biochem. Biophys. Res. Commun. 183, 8-13, 1992
 A:Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type
 A:Reference number: JQ1402; MUID:92181475; PMID:1543512
 A:Accession: JQ1402
 A:Molecule type: DNA
 A:Residues: 1-359 <FUR>
 A:Cross-references: EMBL:Z11162; NID:928709; PID:928710
 A:Experimental source: lymphocyte
 R:Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthalaganti, P.; Kersten, H.; Elshourbagy, N.; G.
 Biochem. Biophys. Res. Commun. 183, 989-995, 1992
 A:Title: Cloning and characterization of a human angiotensin II type 1 receptor.
 A:Reference number: JH0574; MUID:92231907; PMID:1567413
 A:Accession: JH0574
 A:Molecule type: mRNA

JC1194
angiotensin II receptor 1B - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Nov-1999
C:Accession: JC1194; JH0622
R:Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.; J
Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
A:Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (mc
A:Reference number: JC1193; MUID:92359981; PMID:1497638
A:Accession: JC1194
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-359 <YOS>
R:Saemura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 185, 253-259, 1992
A:Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1) i&
A:Reference number: JH0621; MUID:92287102; PMID:1599461
A:Accession: JH0622
A:Molecule type: DNA
A:Residues: 1-6, 'I', 8-165, 'H', 167-172, 'B', 174-204, 'V', 206-231, 'T', 233-238, 'F', 240-359 <E
A:Cross-references: GB:S7491; NID:G249947; PIDN:AAB22270.1; PID:G249948
A:Experimental source: Balb/c
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F:30-53/Domain: transmembrane #status predicted <TM1>
F:65-90/Domain: transmembrane #status predicted <TM2>
F:103-123/Domain: transmembrane #status predicted <TM3>
F:147-166/Domain: transmembrane #status predicted <TM4>
F:195-218/Domain: transmembrane #status predicted <TM5>
F:240-263/Domain: transmembrane #status predicted <TM6>
F:278-300/Domain: transmembrane #status predicted <TM7>
F:4.176.188/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:141/Binding site: phosphate (Thr) (covalent) #status predicted
F:331,338,348/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 59.6%; Score 56; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVTFGEVGNML 18
:|||||::|
Db 31 IPTLYSIIFVVGIFGNL 48

RESULT 26
A48857
angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present i
A:Reference number: A48857; MUID:93236091; PMID:7916579
A:Accession: A48857
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 <BUR>
A:Cross-references: GB:S59041; NID:G299614; PIDN:AAB26239.1; PID:G299615
A:Experimental source: proximal tubule cells
A:Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIPI:129601)
C:Superfamily: vertebrate rhodopsin

Query: 1 LPPYLSLVVFIFGVGNML 18
 : ||||::: ||||
 Db: 31 LFTYSLIFVVGIFGNL 48

Query Match 59.6%; Score 56; DB 2; Length 359;
 Best Local Similarity 50.0%; Pred. NO. 0.18;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

RESULT 27

A42656
 angiotensin II receptor type 1B (AT3) - rat
 N:Alternate names: angiotensin II receptor chain B
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C:Accession: A42656; S20423
 R:Sandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Catt, K.J.
 J. Biol. Chem. 267, 9455-9458, 1992
 A:Title: Cloning and expression of a novel angiotensin II receptor subtype.
 A:Reference number: A42656; MUID:92250585; PMID:1374402
 A:Accession: A42656
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <SAS>
 A:Cross-references: GB:M90065; NID:g202801; PIDN:AAA40704.1; PID:g202802
 A:Experimental source: adrenal cortex
 A:Note: Sequence extracted from NCBI backbone (NCBIN:100262, NCBIP:100268)
 R:Iwai, N.; Inagami, T.
 FEBS Lett. 298, 257-260, 1992
 A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.
 A:Reference number: S20423; MUID:92183879; PMID:1544458
 A:Accession: S20423
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <IWA>
 A:Cross-references: GB:X64052; NID:g57521; PIDN:CAA45410.1; PID:g57522
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 59.6%; Score 56; DB 2; Length 359;
 Best Local Similarity 50.0%; Pred. No. 0.18;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
 : |||::: |||
 Db 31 IPTLYSIIFVVGIFGNSL 48

RESULT 28

SI5403
 angiotensin II receptor type 1 - bovine
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
 C:Accession: SI5403
 R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Haegawa, M.; Matsuda, Y.
 Nature 351, 230-233, 1991
 A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin II receptor.
 A:Reference number: SI5403; MUID:91251900; PMID:2041569
 A:Accession: SI5403
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-359 <SAS>
 A:Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
 C:Superfamily: vertebrate rhodopsin

Query Match 59.6%; Score 56; DB 2; Length 359;
 Best Local Similarity 50.0%; Pred. No. 0.18;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
 : |||::: |||
 Db 31 IPTLYSIIFVVGIFGNSL 48

RESULT 29

I39418
 angiotensin II receptor type 1b - human
 C:Species: Homo sapiens (man)
 C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Nov-1999
 C:Accession: I39418
 R:Kuroda, S.
 Biochem. Biophys. Res. Commun. 199, 467-474, 1994

A:Title: Novel subtype of human angiotensin II type 1 receptor: cDNA cloning and express
 A:Reference number: I39418; MUID:94183213; PMID:8135787
 A:Accession: I39418
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-359 <RES>
 A:Cross-references: GB:D13814; NID:g471120; PIDN:BAA02968.1; PID:g471121
 C:Superfamily: vertebrate rhodopsin

Query Match 59.6%; Score 56; DB 2; Length 359;
 Best Local Similarity 50.0%; Pred. No. 0.18;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
 : |||::: |||
 Db 31 IPTLYSIIFVVGIFGNSL 48

RESULT 30

JH0621
 angiotensin II receptor 1A - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Nov-1999
 C:Accession: JH0621; JC1193
 R:Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
 Biochem. Biophys. Res. Commun. 185, 253-259, 1992
 A:Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1) is
 A:Reference number: JH0621; MUID:92287102; PMID:1599461
 A:Accession: JH0621
 A:Molecule type: DNA
 A:Residues: 1-359 <SAS>
 A:Cross-references: GB:S37484; NID:g249945; PIDN:AAE22269.1; PID:g249946
 A:Experimental source: strain Balb/C
 R:Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.; I
 Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
 A:Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (mc
 A:Reference number: JC1193; MUID:92359981; PMID:1497638
 A:Accession: JC1193
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-6, 'I', 8-19, 'IS', 22-37, 'M', 39-133, 'K', 135-359 <YOS>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot-

Query Match 59.6%; Score 56; DB 2; Length 359;
 Best Local Similarity 50.0%; Pred. No. 0.18;
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
 : |||::: |||
 Db 31 IPTLYSIIFVVGIFGNSL 48

Search completed: March 4, 2004, 18:03:56
 Job time : 10.1837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 5.87755 Seconds
(without alignments)
159.465 Million cell updates/sec

Title: US-10-084-813-11

Perfect score: 94

Sequence: 1 LPPLYSILVIFGFGVGNML 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	94	100.0	352	1	CCR5_GORGO
2	94	100.0	352	1	CCR5_HUMAN
3	94	100.0	352	1	CCR5_HYLLE
4	94	100.0	352	1	CCR5_HYLLM
5	94	100.0	352	1	CCR5_HYLSY
6	94	100.0	352	1	CCR5_PANTR
7	94	100.0	352	1	CCR5_PONPY
8	94	100.0	352	1	CCR2_MACMU
9	94	100.0	373	1	CCR2_MOUSE
10	94	100.0	373	1	CCR2_RAT
11	94	100.0	374	1	CCR2_HUMAN
12	92	97.9	354	1	CCR5_MOUSE
13	92	97.9	354	1	CCR5_RAT
14	90	95.7	352	1	CCR5_CERAE
15	90	95.7	352	1	CCR5_CERP
16	90	95.7	352	1	CCR5_CERTO
17	90	95.7	352	1	CCR5_MACMU
18	90	95.7	352	1	CCR5_PAPHA
19	90	95.7	352	1	CCR5_PYGBI
20	90	95.7	352	1	CCR5_PYGNE
21	90	95.7	352	1	CCR5_TRAFR
22	90	95.7	352	1	CCR5_TRAPH
23	77	81.9	355	1	CCR1_HUMAN
24	77	81.9	355	1	CCR1_MACMU
25	77	81.9	355	1	CCR1_MOUSE
26	77	81.9	359	1	CCR3_MOUSE
27	76	80.9	359	1	CCR3_RAT
28	75	79.8	360	1	CCR4_HUMAN
29	66	70.2	360	1	CCR4_MOUSE
30	65	69.1	355	1	CCR3_MACMU
31	63	67.0	355	1	CCR3_CERAE
32	63	67.0	355	1	CCR3_HUMAN
33	63	67.0	357	1	CCR9_HUMAN

34	63	67.0	369	1	CCR9_MOUSE
35	61	64.9	378	1	CCR6_MOUSE
36	61	64.9	382	1	CCR6_RAT
37	60	63.8	356	1	CCR6_MOUSE
38	60	63.8	361	1	CCR6_HUMAN
39	59	62.8	373	1	CCR6_BOVIN
40	59	62.8	373	1	CCR6_HUMAN
41	59	62.8	373	1	CCR6_MOUSE
42	59	62.8	373	1	CCR6_RAT
43	58	61.7	354	1	CCR1_RAT
44	58	61.7	358	1	CCR3_CAVPO
45	58	61.7	384	1	CCR6_HUMAN
46	57	60.6	352	1	CCR4_CERTO
47	57	60.6	352	1	CCR4_HUMAN
48	57	60.6	352	1	CCR4_MACFA
49	57	60.6	352	1	CCR4_MACMU
50	57	60.6	352	1	CCR4_PAPAN
51	57	60.6	362	1	CCR4_CHICK
52	57	60.6	362	1	CCR4_MELGA
53	57	60.6	367	1	CCR3_MOUSE
54	57	60.6	368	1	CCR3_HUMAN
55	57	60.6	373	1	CCR3_CAVPO
56	56	59.6	192	1	CCR4_SHEEP
57	56	59.6	353	1	CCR4_BOVIN
58	56	59.6	353	1	CCR4_FELCA
59	56	59.6	354	1	CCR1_MOUSE
60	56	59.6	359	1	CCR2_BOVIN
61	56	59.6	359	1	CCR2_CANFA
62	56	59.6	359	1	CCR2_CAVPO
63	56	59.6	359	1	CCR2_HUMAN
64	56	59.6	359	1	CCR2_MERUN
65	56	59.6	359	1	CCR2_MOUSE
66	56	59.6	359	1	CCR2_PANTR
67	56	59.6	359	1	CCR2_PIG
68	56	59.6	359	1	CCR2_RABIT
69	56	59.6	359	1	CCR2_RAT
70	56	59.6	359	1	CCR2_SHEEP
71	56	59.6	359	1	CCR2_HUMAN
72	56	59.6	359	1	CCR2_MOUSE
73	56	59.6	359	1	CCR2_RAT
74	56	59.6	372	1	CCR5_HUMAN
75	56	59.6	374	1	CCR5_MOUSE
76	56	59.6	374	1	CCR5_RAT
77	56	59.6	387	1	CCR5_HUMAN
78	54	57.4	359	1	CCR5_CHICK
79	54	57.4	359	1	CCR5_MELGA
80	53	56.4	354	1	CCR6_HCMVA
81	53	56.4	374	1	CCR6_HUMAN
82	52	55.3	337	1	CCR6_HUMAN
83	52	55.3	342	1	CCR6_CERAE
84	52	55.3	342	1	CCR6_HUMAN
85	52	55.3	342	1	CCR6_MACNE
86	52	55.3	342	1	CCR6_PANTR
87	52	55.3	343	1	CCR6_MACFA
88	52	55.3	343	1	CCR6_MACMU
89	52	55.3	416	1	CCR2_RAT
90	51	54.3	343	1	CCR1_MOUSE
91	51	54.3	349	1	CCR4_RAT
92	51	54.3	359	1	CCR4_MOUSE
93	51	54.3	367	1	CCR6_MOUSE
94	50	53.2	322	1	CCR1_MOUSE
95	50	53.2	363	1	CCR2_MERUN
96	50	53.2	370	1	CCR2_RAT
97	50	53.2	380	1	OPRK_CAVPO
98	50	53.2	380	1	OPRK_HUMAN
99	50	53.2	380	1	OPRK_MOUSE
100	50	53.2	380	1	OPRK_RAT

ALIGNMENTS

RESULT 1

```
CKR5 GORGO
ID CKR5 GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
GN CKR5 OR CMKRS.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268697; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC 1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
CC 1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
DR EMBL; AF005659; AAB62553.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40515 MW; D086FCB9FE5EAC84 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVPIFGVGNML 18
| | | | | | | | | | | | | | | |
DB 33 LPPLSLVPIFGVGNML 50
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RESULT 2

CKR5_HUMAN

```
ID CKR5 HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; O9UPA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CKR5 OR CMKRS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
RT C-C chemokine receptor gene.";
RL Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
RT C-C chemokine receptor (CCRS) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9625970; PubMed=8699119;
RA Combadere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RT RANTES.";
RL J. Leukoc. Biol. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RX Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RX Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RX Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RX Porcel B.M., Dragan Y., Giacalone J., Rae A., Powell E.,
RX Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RX Matanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kubmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201;
RA Mummaidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
RT with 5'-end heterogeneity, dual promoter usage, and evidence for
RT polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).
```


DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 GN C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 OS CCR5 OR CCR5.
 OC Hylobates leucogenys (White-cheeked gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=61853;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 DR EMBL; AF075451; AAD19863.1; -;
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PS00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;
 Query Match 100.0%; Score 94; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LPPLYSLVIFGFGVGNML 18
 DB 33 LPPLYSLVIFGFGVGNML 50
 RESULT 4
 ID_CKRS_HYLM ML STANDARD; PRT; 352 AA.
 AC Q95NC0;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Hylobates moloch (Silvery gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=81572;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 DR EMBL; AF177899; AAK43382.1; -;
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PS00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;
 Query Match 100.0%; Score 94; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LPPLYSLVIFGFGVGNML 18
 DB 33 LPPLYSLVIFGFGVGNML 50
 RESULT 5
 ID_CKRS_HYLS Y STANDARD; PRT; 352 AA.
 AC Q95NC5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKERS.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL: AF177884; AAK43367.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7cm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G PROTEIN RECF 1; 1.
DR PROSITE: PS0262; G PROTEIN RECF 2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW FT DOMAIN 1 30
KW TRANSMEM 31 58
KW DOMAIN 59 68
KW TRANSMEM 69 89
KW DOMAIN 90 102
KW TRANSMEM 103 124
KW DOMAIN 125 141
KW TRANSMEM 142 166
KW DOMAIN 167 198
KW TRANSMEM 199 218
KW DOMAIN 219 235
KW TRANSMEM 236 260
KW DOMAIN 261 277
KW TRANSMEM 278 301
KW DOMAIN 302 352
KW DISULFID 101 178
KW MOD_RES 3 3
KW MOD_RES 10 10
KW MOD_RES 14 14
KW SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;
Query Match 100.0%; Score 94; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 5,1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LPPLYSIVFIFGVGNML 18
Db 33 LPPLYSIVFIFGVGNML 50
RESULT 6
CKR5_PANTR
ID CKR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

GN CCR5 OR CMKERS.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC [2]
RP SEQUENCE FROM N.A.
RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
RA Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
CC [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host.";
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
CC [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC [6]
RP SEQUENCE FROM N.A.
RX Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL: AF005663; AAB62557.1; -;
DR EMBL: U94329; AAB58446.1; -;
DR EMBL: AF011542; AAB65742.1; -;
DR EMBL: U97666; AAC51670.1; -;
DR EMBL: AF011540; AAB65740.1; -;
DR EMBL: U89757; AAC03717.1; -;
DR EMBL: AF177894; AAK43377.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7cm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G PROTEIN RECF 1; 1.
DR PROSITE: PS0262; G PROTEIN RECF 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

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FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 14 10 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF. 1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33B698B80FE34C CRC64;

Query Match 100.0%; Score 94; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
DB 33 LPPLYSLVFIFGFVGNML 50

RESULT 7
CKR5_PONPY
ID CKR5_PONPY STANDARD; PRT; 352 AA.
AC 097881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CKR5R.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder C.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075446; AAD19858.1; -
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.
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DR PROSITE; PS00262; G_PROTEIN_RECEPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF659A CRC64;

Query Match 100.0%; Score 94; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
DB 33 LPPLYSLVFIFGFVGNML 50

RESULT 8
CKR2_MACMU
ID CKR2_MACMU STANDARD; PRT; 360 AA.
AC 018793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN CCR2 OR CKR2R.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=O18793-1; Sequence=Displayed;
CC Name=A;
CC IsoId=O18793-2; Sequence=Not described;
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC -----
DR EMBL; AF013958; AAD11572.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Alternative splicing.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 136 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC... ) (POTENTIAL).
FT MOD RES 26 26 SULFATION (BY SIMILARITY).
FT DISULFID 113 190 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 100.0%; Score 94; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGFVGNML 18
Db 45 LPPLYSLVFIFGFVGNML 62

RESULT 9
CCR2_MOUSE STANDARD; PRT; 373 AA.
AC P15683; Q61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CCR-2) (CCR-2) (CCR2)
DE (JE/FIC receptor) (MCP-1 receptor).
GN CCR2 OR CMKBR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Goelling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT receptors: evidence for two closely linked C-C chemokine
RT J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA MEDLINE=96216064; PubMed=8662823;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
RT the C-C chemokines JE and EIC".
RL J. Biol. Chem. 271:11603-11606(1996).
RN [3]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97026720; PubMed=8872898;
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA Post T.W., Gerard C., Dorf M.E.;
RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
RT transcriptase-polymerase chain reaction does not detect mRNA for the
RT KC or new MCP-1 receptor."
RL J. Neurosci. Res. 45:382-391(1996).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; U47035; AAC52453.1; -.
DR EMBL; U51717; AAC52557.1; -.
DR EMBL; U56819; AAC52784.1; -.
DR MGD; MGI-106185; Ccr2.
DR GO; GO:0016493; P:C-C chemokine receptor activity; IDA.
DR GO; GO:0019955; F:Cytokine binding; IPI.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
DR GO; GO:0030097; P:hemopoiesis; IMP.
DR GO; GO:0006959; P:humoral immune response; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0030334; P:regulation of cell migration; IMP.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 83 1 (POTENTIAL).
FT DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 94 114 2 (POTENTIAL).
FT DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 128 149 3 (POTENTIAL).
FT DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 239 5 (POTENTIAL).
FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 281 6 (POTENTIAL).
FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 299 322 7 (POTENTIAL).
FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203 BY SIMILARITY.
FT CONFLICT 39 39 Y -> H (IN REF. 1).
FT CONFLICT 184 184 A -> G (IN REF. 1).
FT CONFLICT 264 264 V -> G (IN REF. 1).
SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 100.0%; Score 94; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGFVGNML 18
Db 58 LPPLYSLVFIFGFVGNML 75

RESULT 10
CCR2_RAT STANDARD; PRT; 373 AA.
ID CCR2_RAT

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AC 055193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 2 (CCR-2) (CCR-2) (CCR2)
GN CCR2 OR CMKBR2
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafian M.A., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streif W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured gila and rat experimental
RT allergic encephalomyelitis."
RL J. Neuroimmunol. 86:1-12(1998).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (PIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC macrophages.
CC -!- INDUCTION: In animals in which experimental allergic
CC encephalomyelitis (EAE) has been induced.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U77349; AAC03242.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 60
FT TRANSMEM 61 81
FT DOMAIN 82 91
FT TRANSMEM 92 112
FT DOMAIN 113 128
FT TRANSMEM 129 149
FT DOMAIN 150 170
FT TRANSMEM 171 191
FT DOMAIN 192 220
FT TRANSMEM 221 241
FT DOMAIN 242 256
FT TRANSMEM 257 277
FT DOMAIN 278 301
FT TRANSMEM 302 322
FT DOMAIN 323 373
FT DISULFID 126 203
SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5DFD09 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLSLVIFGFVGNML 18
Db 58 LPPLSLVIFGFVGNML 75

RESULT 11
CCR2_HUMAN

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ID CCR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE C-C chemokine receptor type 2 (CCR-2) (CCR-2) (CCR2)
DE C-C chemokine receptor type 2 (CCR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
DE CCR2 OR CMKBR2
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195821; PubMed=8146186;
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94324942; PubMed=8048929;
RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
RT chemoattractant protein 1 receptor."
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97150864; PubMed=8995400;
RA Wong L.-M., Myers S.J., Teou C.-L., Gosling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RT carboxyl-terminal tail in receptor trafficking."
RL J. Biol. Chem. 272:1038-1045(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Guoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU.355.
RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX MEDLINE=20501139; PubMed=11046064;
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RA Chakravarty L., Kolattukudy P.E.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RT region."
RL J. Immunol. 165:5295-5303(2000).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P41597-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P41597-2; Sequence=VSP_001893;
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC

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EMBL; U03882; AAA19119.1; -
EMBL; U03905; AAA19120.1; -
EMBL; D29984; BAA06253.1; -
EMBL; U80924; AAC51637.1; -
EMBL; U80924; AAC51636.1; -
EMBL; U95626; AAB57791.1; -
EMBL; U95626; AAB57792.1; -
EMBL; A8545480; AAX16400.1; -
PIR; J38450; I38450.
PIR; JC2443; JC2443.
PDB; 1KAD; 14-AUG-02.
PDB; 1KPI; 23-JAN-02.
Genew; HGNC:1603; CCR2.
MIM; 601267; -
GO; GO:0005887; C: integral to plasma membrane; TAS.
GO; GO:0005625; C: soluble fraction; TAS.
GO; GO:0004950; F: chemokine receptor activity; TAS.
GO; GO:0006960; P: antimicrobial humoral response (sensu Inver. .); TAS.
GO; GO:0006968; P: cellular defense response; TAS.
GO; GO:0005935; P: chemotaxis; TAS.
GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
GO; GO:0006954; P: inflammatory response; TAS.
GO; GO:0007125; P: invasive growth; TAS.
GO; GO:0007259; P: JAK-STAT cascade; TAS.
GO; GO:0007194; P: negative regulation of adenylate cyclase ac. .; TAS.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PF00001; 7tm.1; 1.
PRINTS; PRO0237; GPCR_RHODOPSIN.
PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
Polymorphism; Alternative splicing; 3D-structure.
DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
TRANSMEM 43 70 1 (POTENTIAL).
DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
TRANSMEM 81 100 2 (POTENTIAL).
DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
TRANSMEM 115 136 3 (POTENTIAL).
DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
TRANSMEM 154 178 4 (POTENTIAL).
DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
TRANSMEM 207 226 5 (POTENTIAL).
DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
TRANSMEM 244 268 6 (POTENTIAL).
DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
TRANSMEM 286 309 7 (POTENTIAL).
DOMAIN 310 374 N-LINKED (GLCNAC. .) (POTENTIAL).
SULFATION.
BY SIMILARITY.
SLFHIALGCRAPLQKPCVGGPGVGRKKNVKTQGLDGR
GKGSGIRAPASLQDKGA -> RYLSVFFKKHTRFKC
QCPVFRYTDVGTSTNPTSTGEQVSAGL (in isoform B).
/FTid=vsp.001893.
V -> I (in dbSNP:1799864).
/FTid=VAR_014339.
G -> E.
FT MOD RES 26 26
FT DISULFID 113 190
FT VARSPLIC 314 374
SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;

Query Match 100.0%; Score 94; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLSLVPIFGVGNML 18
Db 45 LPPLSLVPIFGVGNML 62
RESULT 12
CKR5 MOUSE
ID CKR5 MOUSE STANDARD; PRT: 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
DE alpha receptor).
GN CKR5 OR CXCR5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT 1alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=862890;
RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451 (1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RX Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RN Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CKR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656 (1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=97404635; PubMed=9261347;
RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharon M., Cen Y.H.,
RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT "Two distinct CKR5 domains can mediate coreceptor usage by human
RT immunodeficiency virus type 1.";
RL J. Virol. 71:6305-6314 (1997).
RN [6]
RP SEQUENCE FROM N.A.
RA Guo B., Kudo K., Harada A., Matsushima K.;
RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -| FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -| SUBCELLULAR LOCATION: Integral membrane protein.
CC -| TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -| SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; U47036; AAC52454.1; -
DR EMBL; X94151; CAA63867.1; -
DR EMBL; U68565; AAB37273.1; -
DR EMBL; U83327; AAC33386.1; -
DR EMBL; AF022990; AAC53389.1; -
DR EMBL; AF019772; AAB71183.1; -
DR EMBL; D83648; BAA12024.1; -
DR MGD; MG1:107182; Ccr5.
DR GO; GO:0016493; F-C-C chemokine receptor activity; IDA.
DR GO; GO:0006952; P:defense response; IMP.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 60 1 (POTENTIAL).
FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 71 91 2 (POTENTIAL).
FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 105 126 3 (POTENTIAL).
FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 168 4 (POTENTIAL).
FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 5 (POTENTIAL).
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 262 6 (POTENTIAL).
FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 280 303 7 (POTENTIAL).
FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
FT DISULFID 103 180 BY SIMILARITY.
FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 11 11 I -> S.
FT VARIANT 62 62 K -> R.
FT VARIANT 66 66 V -> M.
FT VARIANT 97 97 I -> V.
FT VARIANT 109 109 V -> L.
FT VARIANT 156 156 V -> A.
FT VARIANT 160 160 F -> S.
FT VARIANT 185 185 P -> L.
FT VARIANT 213 213 I -> V.
FT VARIANT 318 318 I -> M.
FT VARIANT 337 337 V -> A.
FT CONFLICT 3 3 F -> L (IN REF. 2).
FT CONFLICT 80 80 L -> F (IN REF. 2).
FT CONFLICT 145 145 N -> I (IN REF. 5).
FT CONFLICT 190 190 H -> Y (IN REF. 3).
FT CONFLICT 208 208 P -> S (IN REF. 1).
SQ SEQUENCE 354 AA; 40863 MW; B4ACB942E88F9CF0 CRC64;

Query Match 97.9%; Score 92; DB 1; Length 354;
Best Local Similarity 94.4%; Pred. No. 1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
|||||
Db 35 LPPLYSLVIFGFGVGNMW 52

RESULT 13
CKR5 RAT STANDARD; PRT; 354 AA.
AC O08556;
DT 01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
alpha receptor).
GN CCR5 OR CCR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=98334064; PubMed=9670989;
RA Splenis O., Gourmal N., Bodde H.W.G.M., Sauter A., Fiebich B.L.,
Berger M., Gebicke-Haerter P.J.;
RT Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RL J. Neurosci. Res. 53:16-28 (1998).
[2]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12 (1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
increasing the intracellular calcium ions level.
CC MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).

EMBL; Y12009; CAA72737.1; -
DR EMBL; U77350; AAC03243.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; Glycoprotein.
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 33 60 1 (POTENTIAL).
FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 71 91 2 (POTENTIAL).
FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 105 126 3 (POTENTIAL).
FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 144 168 4 (POTENTIAL).
FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 5 (POTENTIAL).
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 262 6 (POTENTIAL).
FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 280 303 7 (POTENTIAL).
FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
FT DISULFID 103 180 BY SIMILARITY.
FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 354 AA; 41030 MW; 77ED368AA4C86BD CRC64;

Query Match 97.9%; Score 92; DB 1; Length 354;
Best Local Similarity 94.4%; Pred. No. 1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18

```

Db      35 LPPLSLVFIKFGVGNM 52
|||||
RESULT 14
ID      CKR5 CERAE      STANDARD;      PRT;      352 AA.
AC      P56493;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN      CKR5 OR CMKR5.
OS      Cercopithecus aethiops (Green monkey) (Grivet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=9534;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RX      MEDLINE=98001387; PubMed=9343222;
RA      Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT      "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT      implicate specific amino acids in infections by simian and human
RT      immunodeficiency viruses.";
RL      J. Virol. 71:8642-8656(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT      "CDNA sequence of African green monkey CCR-5 chemokine receptor
RT      gene.";
RL      Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC      MIP-1-beta and RANTES and subsequently transduces a signal by
CC      increasing the intracellular calcium ions level. May play a role
CC      in the control of granulocytic lineage proliferation or
CC      differentiation.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; U83324; AAC51795.1; -
DR      EMBL; U83325; AAC51796.1; -
DR      EMBL; AB015944; BAA31328.1; -
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00003; 7tm1; 1.
DR      PRINTS; P00037; GPCRHHODPSN.
DR      PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR      PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW      Polymorphism.
FT      DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 31 58 1 (POTENTIAL).
FT      DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 69 89 2 (POTENTIAL).
FT      DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 103 124 3 (POTENTIAL).
FT      DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 142 166 4 (POTENTIAL).
FT      DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 199 218 5 (POTENTIAL).
FT      DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 236 260 6 (POTENTIAL).
FT      DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 278 301 7 (POTENTIAL).

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FT      DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT      DISULPID 101 178 BY SIMILARITY.
FT      MOD RES 3 SULFATION (BY SIMILARITY).
FT      MOD RES 10 10 SULFATION (BY SIMILARITY).
FT      MOD RES 15 15 SULFATION (BY SIMILARITY).
FT      VARIANT 14 14 N -> Y.
FT      VARIANT 352 352 F -> L.
SQ      SEQUENCE 352 AA; 40561 MW; 7F52B690C72EC29A CRC64;

Query Match      95.7%; Score 90; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLSLVFIKFGVGNM 18
DB      33 LPPLSLVFIKFGVGNM 50

RESULT 15
ID      CKR5 CERPY      STANDARD;      PRT;      352 AA.
AC      Q9TV42;
DT      15-MAR-2004 (Rel. 43, Created)
DT      15-MAR-2004 (Rel. 43, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN      CKR5 OR CMKR5.
OS      Cercopithecus pygerythrus (Vervet monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=60710;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=100;
RX      MEDLINE=99335215; PubMed=10408730;
RA      Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RA      Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT      "Mutations in CCR5-coding sequences are not associated with SIV
RT      carrier status in African nonhuman primates.";
RT      AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC      -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC      MIP-1-beta and RANTES and subsequently transduces a signal by
CC      increasing the intracellular calcium ions level. May play a role
CC      in the control of granulocytic lineage proliferation or
CC      differentiation.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; AF035222; AAD44015.1; -
DR      InterPro; IPR000276; GPCR_Rhodopsn.
DR      Pfam; PF00001; 7tm1; 1.
DR      PRINTS; P00037; GPCRHHODPSN.
DR      PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR      PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT      DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 31 58 1 (POTENTIAL).
FT      DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 69 89 2 (POTENTIAL).
FT      DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 103 124 3 (POTENTIAL).
FT      DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 142 166 4 (POTENTIAL).
FT      DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3D80 CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
Db 33 LPPLYSLVIFGFVGNIL 50

RESULT 16
CKR5_CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVem isolates use the CKR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVem, HIV-2, and SIVmac."
RL Virology 246:113-124(1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro: IPR000276; GPCR_Rhodop.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor, Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 087).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 089).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47B49CA CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
Db 33 LPPLYSLVIFGFVGNIL 50

RESULT 17
CKR5_MACMU STANDARD; PRT; 352 AA.
AC P79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544; 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239."
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CKR5 as a coreceptor for entry."
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;

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RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven thesaurus macaque chemokine
 RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mullatta, M.fascicularis, and M.nemestrina;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC EMBL; U77672; AAC51109.1; -
 CC EMBL; U77673; AAC51158.1; -
 CC EMBL; U96762; AAC34132.1; -
 CC EMBL; AF005660; AAB62554.1; -
 CC EMBL; AF005661; AAB62555.1; -
 CC EMBL; AF005662; AAB62556.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 59 68 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 69 89 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 90 102 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 103 124 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 261 277 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 278 301 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 302 352 BY SIMILARITY.
 FT DISULFID 101 178 SULFATION (BY SIMILARITY).
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 241 241 M -> I (IN REF. 3).
 FT CONFLICT 292 292 I -> M (IN REF. 3).
 SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best local similarity 94.4%; Pred. No. 2.1e-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPLYSLVFIQFVGNNL 18

Db 33 LPLYSLVFIQFVGNNL 50
 |||||
 RESULT 18
 CCR5_PAPHA
 ID CCR5_PAPHA STANDARD; PRT; 352 AA.
 AC P56441;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9557, 9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Sakaena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
 RT "Species-specific changes in the CCR5 gene from African and Asian
 RL AIDS Res. Hum. Retroviruses 15:479-483 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.anubis;
 RA Benton P.A., Timaner D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC EMBL; AF005658; AAB62552.1; -
 CC EMBL; AF105287; AAD20556.1; -
 CC EMBL; AF105288; AAD20557.1; -
 CC EMBL; AF105289; AAD20558.1; -
 CC EMBL; AF105290; AAD20559.1; -
 CC EMBL; AF023452; AAC63830.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 352 AA; 40489 MW; 5E15049BA1FE8B2 CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2.1e-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGVGNML 18
 |||||:|||||:
 Db 33 LPPLYSLVIFGVGNIL 50

RESULT 19
 CKRS PYGBI
 ID CKRS PYGBI STANDARD; PRT; 352 AA.
 AC O97880;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
 GN CCR5 OR CMKRS5.
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 OX NCBI_TaxID=61621;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154 (1999).
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF075445; AAD19857.1;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm1.1;
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G PROTEIN RECEPT F1.1; 1.
 CC PROSITE; PS0262; G PROTEIN RECEPT F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2.1e-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGVGNML 18
 |||||:|||||:
 Db 33 LPPLYSLVIFGVGNIL 50

RESULT 20
 CKRS PYGNE
 ID CKRS PYGNE STANDARD; PRT; 352 AA.
 AC O97882;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS).
 GN CCR5 OR CMKRS5.
 OS Pygathrix nemaeus (Dove langur).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 OX NCBI_TaxID=54133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154 (1999).
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF075448; AAD19860.1;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm1.1;
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G PROTEIN RECEPT F1.1; 1.
 CC PROSITE; PS0262; G PROTEIN RECEPT F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40532 MW; FB4F9D98D3B3B861 CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2.le-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
 DB 33 LPPLYSLVFIQFGVGNIL 50

RESULT 21

ID_CKRS_TRAFR STANDARD; PRT; 352 AA.
 AC O97878;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Trachypithecus.
 OX NCBI_TaxID=54180;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416436; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF075442; AAD19854.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PS00237; GPCRHOOPSN.
 DR PROSITE; PR00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40496 MW; 4366FI48C255938F CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2.le-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
 DB 33 LPPLYSLVFIQFGVGNIL 50

RESULT 22

ID_CKRS_TRAPH STANDARD; PRT; 352 AA.
 AC O97879;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Trachypithecus phayrei (Phayre's leaf monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Trachypithecus.
 OX NCBI_TaxID=61618;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF075443; AAD19855.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PS00237; GPCRHOOPSN.
 DR PROSITE; PR00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT TRANSMEM 59 68
 FT TRANSMEM 69 88
 FT TRANSMEM 89 98
 FT TRANSMEM 99 102
 FT TRANSMEM 103 124
 FT TRANSMEM 125 141
 FT TRANSMEM 142 166
 FT TRANSMEM 167 198
 FT TRANSMEM 199 218
 FT TRANSMEM 219 235
 FT TRANSMEM 236 260
 FT TRANSMEM 261 277
 FT TRANSMEM 278 301
 FT TRANSMEM 302 352
 FT DISULFID 101 178
 FT MOD RES 3 3
 FT MOD RES 10 10
 FT MOD RES 14 14
 FT MOD RES 15 15
 SQ SEQUENCE 352 AA; 40509 MW; 4366FT148D3A5938F CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2.1e-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
 |||||
 DB 33 LPPLYSLVFIFGVGNIL 50

RESULT 23
 CKR1 HUMAN
 ID CKR1 HUMAN STANDARD; PRT; 355 AA.
 AC P32246;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
 DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
 DE (RANTES-R) (HM145) (LD78 receptor).
 GN CCRI OR CMKRI OR CMKRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93161416; PubMed=7679328;
 RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
 RT "Molecular cloning, functional expression, and signaling
 RT characteristics of a C-C chemokine receptor.";
 RL Cell 72:415-425(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93240122; PubMed=7683036;
 RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
 RA Murphy P.M.;
 RT "Structure and functional expression of the human macrophage
 RT inflammatory protein 1 alpha/RANTES receptor.";
 RL J. Exp. Med. 177:1421-1427(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Monocytes;
 RC MEDLINE=94092629; PubMed=7505609;
 RA Nomura H., Nielsen B.W., Matsushima K.;
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
 RT leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-

CC beta or MCP-1 and subsequently transduces a signal by increasing
 CC the intracellular calcium ions level. Responsible for affecting
 CC stem cell proliferation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
 CC cells.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; L09230; AAA58408.1; -;
 CC EMBL; L10918; AAA36543.1; -;
 CC EMBL; D10925; BAA01723.1; -;
 CC PIR; A45177; A45177.
 CC Genew; HGNC:1602; CCR1.
 CC MIM; 601159; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004950; F:chemokine receptor activity; TAS.
 CC GO; GO:0007155; P:cell adhesion; TAS.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0006935; P:chemotaxis; TAS.
 CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
 CC GO; GO:0006955; P:immune response; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC GO; GO:0007125; P:invasive growth; TAS.
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm.1.1.
 CC PRINTS; PR00237; GPCRHOPOPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 34
 FT TRANSMEM 35 60
 FT TRANSMEM 61 64
 FT TRANSMEM 65 91
 FT TRANSMEM 92 107
 FT TRANSMEM 108 129
 FT TRANSMEM 130 146
 FT TRANSMEM 147 171
 FT TRANSMEM 172 197
 FT TRANSMEM 198 223
 FT TRANSMEM 224 239
 FT TRANSMEM 240 264
 FT TRANSMEM 265 281
 FT TRANSMEM 282 305
 FT TRANSMEM 306 355
 FT CARBOHYD 5 5
 FT DISULFID 106 183
 FT CONFLICT 337 337
 SQ SEQUENCE 355 AA; 41172 MW; B2C10FFED275985 CRC64;

Query Match 81.9%; Score 77; DB 1; Length 355;
 Best Local Similarity 77.8%; Pred. No. 0.00019;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
 |||||
 DB 37 LPPLYSLVFIFGVGNIL 54

RESULT 24
 CKR1 MACMU
 ID CKR1 MACMU STANDARD; PRT; 355 AA.
 AC P56482;
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-

DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1).
GN CCR1 OR CCR1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF017282; AAB70526.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34
FT TRANSMEM 35 60
FT DOMAIN 61 64
FT TRANSMEM 65 91
FT DOMAIN 92 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT TRANSMEM 147 171
FT DOMAIN 172 197
FT TRANSMEM 198 223
FT DOMAIN 224 239
FT TRANSMEM 240 264
FT DOMAIN 265 281
FT TRANSMEM 282 305
FT DOMAIN 306 355
FT CARBOHYD 106 5
FT DISULFID 106 183
SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;
Query Match 81.9%; Score 77; DB 1; Length 355;
Best Local Similarity 77.8%; Pred. No. 0.00019;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LPPLYSLVIFGVGNML 18
Db 37 LPPLYSLVIFGVGNML 54
RESULT 25
ID CCR1 MOUSE
AC P51675; Q91VP9;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R).
GN CCR1 OR CCR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV; TISSUE=Peritoneal macrophage;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
receptors.";
RL J. Immunol. 155:5299-5305(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
beta chemokine receptor-like genes, including the gene for a
functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smaluk D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in the heart, spleen, lung,
CC peritoneal exudate cells and leukocytes.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U29678; AAA86119.1; -
DR EMBL; U28404; AAA89153.1; -
DR EMBL; BC011092; AAA11092.1; -
DR PIR; I49339; I49339.

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DR MGD; MGI:104618; Cor1.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0030595; P:immune cell chemotaxis; IDA.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0003099; P:myeloid blood cell differentiation; IMP.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 325 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 55 55 M -> V (IN REF. 2 AND 3).
FT CONFLICT 149 149 L -> F (IN REF. 3).
FT CONFLICT 278 278 H -> Q (IN REF. 3).
SQ SEQUENCE 355 AA; 40901 MW; FCE9FFF70B6F38B1 CRC64;

Query Match 81.9%; Score 77; DB 1; Length 355;
Best Local Similarity 83.3%; Pred. No. 0.00019;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18
Db 37 LPPLYSLVIFGVGNML 54

RESULT 26
CKR3_MOUSE
ID CKR3_MOUSE STANDARD; PRT; 359 AA.
AC P51678.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3)
DE (CKR3) (CKR3) (Macrophage inflammatory protein-1 alpha receptor-like
DE 2) (MIP-1 alpha RL2)
GN CKR3 OR CMKBR3 OR CMKBR1L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors."
RL J. Immunol. 155:5299-5305 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a

```

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RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501 (1995).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
CC amounts in leukocytes.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U29677; AAA86118.1; -.
CC EMBL; U28406; AAA89155.1; -.
CC MGD; MGI:104618; Cor3.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006935; P:chemotaxis; IDA.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 64 1 (POTENTIAL).
FT DOMAIN 65 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 95 2 (POTENTIAL).
FT DOMAIN 96 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 227 5 (POTENTIAL).
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 270 270 R -> S (IN REF. 2).
SQ SEQUENCE 359 AA; 41825 MW; AC11ED6E283CEAF CRC64;

Query Match 81.9%; Score 77; DB 1; Length 359;
Best Local Similarity 77.8%; Pred. No. 0.00019;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18
Db 41 LPPLYSLVIFGVGNML 58

RESULT 27
CKR3_RAT
ID CKR3_RAT STANDARD; PRT; 359 AA.
AC O54814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CCR3).
GN CKR3 OR CMKBR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

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RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX STRAIN=Wistar; TISSUE=Spleen;
RA MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RA "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:11-12(1998).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
CC microglia.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC -----
DR EMBL; AF003954; AAC03337.1; -.
DR EMBL; Y13400; CAA73830.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 POTENTIAL.
FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 95 POTENTIAL.
FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 POTENTIAL.
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 POTENTIAL.
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 227 POTENTIAL.
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 309 POTENTIAL.
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 164 164 F -> L (IN REF. 2).
SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;

Query Match 80.9%; Score 76; DB 1; Length 359;
Best Local Similarity 77.8%; Pred. NO. 0.00027;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LPPLSLVFIKFGVGNML 18
DB 41 LPPLSLVFIKGLGNM 58
|||||
|||||

RESULT 28
CKR4_HUMAN
ID CKR4_HUMAN STANDARD; PRT; 360 AA.
AC P51679; Q9ULY6; Q9ULY7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 4 (C-C CKR-4) (CC-CKR-4) (CCR-4) (CCR4) (KS-5).
```

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GN CCR4 OR CMKBR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=95370289; PubMed=7642634;
RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
RA Proudfoot A.E.I., Wells T.N.C.;
RA "Molecular cloning and functional expression of a novel CC chemokine
RT receptor cDNA from a human basophilic cell line.";
RL J. Biol. Chem. 270:19495-19500(1995).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
RX MEDLINE=21040311; PubMed=11196669;
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawaasaki H.,
RA Hirai K., Tokunaga K.;
RA "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RA "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=97313486; PubMed=9169480;
RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
RA "The T cell-directed CC chemokine TARC is a highly specific
RT biological ligand for CC chemokine receptor 4.";
RL J. Biol. Chem. 272:15036-15042(1997).
RN [5]
RP FUNCTION.
RX MEDLINE=98104168; PubMed=9430724;
RA Imai T., Chantray D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
RA Yoshie O., Gray P.W.;
RA "Macrophage-derived chemokine is a functional ligand for the CC
RT chemokine receptor 4.";
RL J. Biol. Chem. 273:1764-1768(1998).
RN [6]
RP FUNCTION.
RX MEDLINE=99394604; PubMed=10466728;
RA Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,
RA Andrew D.P., Warke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
RA "The chemokine receptor CCR4 in vascular recognition by cutaneous but
RT not intestinal memory T cells.";
RL Nature 400:776-780(1999).
RN [7]
RP FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
RX MEDLINE=20219238; PubMed=10754297;
RA Ingberdingen M., Damaj B., Maghazachi A.A.;
RA "Human NK cells express CC chemokine receptors 4 and 8 and respond to
RT thymus and activation-regulated chemokine, macrophage-derived
RT chemokine, and I-309.";
RL J. Immunol. 164:4048-4054(2000).
RN -!- FUNCTION: High affinity receptor for the C-C type chemokines
CC TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
CC mediated by G(i) proteins which activate a phosphatidylinositol-
CC calcium second messenger system. Can function as a chemoattractant
CC homing receptor on circulating memory lymphocytes and as a
CC coreceptor for some primary HIV-2 isolates. In the CNS, could
CC mediate hippocampal-neuron survival.
RN -!- SUBCELLULAR LOCATION: Integral membrane protein.
RN -!- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in
CC peripheral blood leukocytes, including T cells, mostly cd4+ cells,
CC and basophils, and in platelets; at lower levels, in the spleen
CC and in monocytes. Detected also in macrophages, IL-2-activated
CC natural killer cells and skin-homing memory T cells, mostly the
CC ones expressing the cutaneous lymphocyte antigen (CLA). Expressed
CC in brain microvascular and coronary artery endothelial cells.
```

CC -!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X85740; CAA59743.1; --
CC EMBL: AB023888; BAA86965.1; --
CC EMBL: AB023889; BAA86966.1; --
CC EMBL: AB023890; BAA86967.1; --
CC EMBL: AB023891; BAA86968.1; --
CC EMBL: AB023892; BAA86969.1; --
CC EMBL: AB023893; BAA86970.1; --
CC EMBL: AY322539; AAP84352.1; --
CC PIR: A57160; A57160.
CC Genew: HGNC:1605; CCR4.
CC MIM: 604936; --
CC GO: GO:0005887; C:integral to plasma membrane; TAS.
CC GO: GO:0004950; F:chemokine receptor activity; TAS.
CC GO: GO:0006935; P:chemotaxis; TAS.
CC GO: GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
CC GO: GO:0006955; P:immune response; TAS.
CC GO: GO:0006954; P:inflammatory response; TAS.
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC Pfam: PF00001; 7tm1; 1.
CC PRINTS: PR00237; GPCR_RHODOPSIN.
CC PROSITE: PS00237; G_PROTEIN_RECP_F1.1; 1.
CC PROSITE: PS0262; G_PROTEIN_RECP_F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Polymorphism.
CC DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 67 1 (POTENTIAL).
CC DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 78 98 2 (POTENTIAL).
CC DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 112 133 3 (POTENTIAL).
CC DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 151 175 4 (POTENTIAL).
CC DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 207 226 5 (POTENTIAL).
CC DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 243 267 6 (POTENTIAL).
CC DOMAIN 268 284 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 285 308 7 (POTENTIAL).
CC DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 110 187 BY SIMILARITY.
CC FT VARIANT 130 130 L -> V.
CC FT VARIANT 178 178 /FTID=VAR_010669.
CC FT VARIANT 178 178 C -> S.
CC FT VARIANT 178 178 /FTID=VAR_010670.
CC SEQUENCE 360 AA; 41402 MW; 51EBE12AD1FAFBF CRC64;
CC
CC Query Match 79.8%; Score 75; DB 1; Length 360;
CC Best Local Similarity 81.2%; Pred. No. 0.00039;
CC Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 1 LPPLYSIVRIFGFCVGN 16
CC DB 42 LPPLYSIVRIFGFCVGN 57
CC
CC RESULT 29
CC CKR4 MOUSE
CC ID CKR4 MOUSE STANDARD; PRT; 360 AA.
CC AC P51680;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4).
GN CCR4 OR CMKBR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96136324; PubMed=8573157;
RA Hoogwerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Molecular cloning of murine CC CKR-4 and high affinity binding of
RT chemokines to murine and human CC CKR-4.";
RL Biochem. Biophys. Res. Commun. 218:337-343(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;
RX MEDLINE=97335974; PubMed=9192769;
RA Young B.-S., Kim S.-H., Lyu M.S., Kozak C.A., Taub D.D., Kwon B.S.;
RT "Molecular cloning and characterization of a cDNA, CHEW1, encoding a
RT chemokine receptor with a homology to the human C-C chemokine
RN receptor, CCR-4.";
RL Blood 89:4448-4460(1997).
RN [3]
RP FUNCTION.
RC MEDLINE=20273981; PubMed=10811868;
RA Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced
RT endotoxic shock.";
RL J. Exp. Med. 191:1755-1764(2000).
CC -!- FUNCTION: High affinity receptor for the C-C type chemokines
CC TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
CC mediated by G(i) proteins which activate a phosphatidylinositol-
CC calcium second messenger system. Could play a role in
CC lipopolysaccharide (LPS)-induced endotoxic shock. In the CNS,
CC could mediate hippocampal-neuron survival.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the thymus, macrophages and T-
CC and B-cells.
CC -!- DEVELOPMENTAL STAGE: Low expression at 7.5 dpc and 12.5 dpc in the
CC yolk sac.
CC -!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: X90862; CAA62372.1; --
CC EMBL: U15208; AAA92582.1; --
CC PIR: JC4587; JC4587.
CC MGD: MGI:107824; Ccr4.
CC GO: GO:0016493; F:C-C chemokine receptor activity; IMP.
CC GO: GO:0006935; P:chemotaxis; IMP.
CC GO: GO:0006954; P:inflammatory response; IMP.
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC Pfam: PF00001; 7tm1; 1.
CC PRINTS: PR00237; GPCR_RHODOPSIN.
CC PROSITE: PS00237; G_PROTEIN_RECP_F1.1; 1.
CC PROSITE: PS0262; G_PROTEIN_RECP_F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation.
CC DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 67 1 (POTENTIAL).
CC FT TRANSMEM 40 67 1 (POTENTIAL).

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FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 78 98 2 (POTENTIAL).
FT DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 243 267 6 (POTENTIAL).
FT DOMAIN 268 284 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 285 308 7 (POTENTIAL).
FT DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 343 346 POLY-SER.
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 4 4 T -> I (IN REF. 2).
FT CONFLICT 145 145 S -> T (IN REF. 2).
FT CONFLICT 181 181 E -> Q (IN REF. 2).
FT CONFLICT 205 205 E -> D (IN REF. 2).
FT CONFLICT 221 221 W -> C (IN REF. 2).
FT CONFLICT 241 241 V -> L (IN REF. 2).
FT CONFLICT 246 246 G -> A (IN REF. 2).
FT CONFLICT 293 293 G -> A (IN REF. 2).
FT CONFLICT 311 311 F -> S (IN REF. 2).
SQ SEQUENCE 360 AA; 41462 MW; 97BDBAC9D259AE3 CRC64;

Query Match 70.2%; Score 66; DB 1; Length 360;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVN 16
DB 42 LPPLYSLVIFLGLFVN 57

RESULT 30
CKR3 MACMU STANDARD; PRT; 355 AA.
AC P564B3;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CCR3).
GN CCR3 OR CMKBR3. (Rhesus macaque).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118446; PubMed=9454694;
RA Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;
RT "The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
RT for HIV-2, but not for HIV-1."
RL Virology 240:213-220(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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DR EMBL; AF017283; BAB70527.1; -.
DR EMBL; Y13776; CAAT4107.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 180 180 K -> E (IN REF. 2).
FT CONFLICT 202 202 K -> R (IN REF. 2).
SQ SEQUENCE 355 AA; 40805 MW; E271FIE694970D9F CRC64;

Query Match 69.1%; Score 65; DB 1; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.012;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVNML 18
DB 37 VPPLYSLVFMVGLGNV 54
:|||||:|:|:|:
:|||||:|:|:|:

Search completed: March 4, 2004, 18:00:02
Job time : 6.07755 secs
```

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 29.0204 Seconds
(without alignments)
195.701 Million cell updates/sec

Title: US-10-084-813-11

Perfect score: 94

Sequence: 1 LPPLYSLVFIFGVGNML 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mic.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp Vertebrate.*
- 14: sp Unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	215	4	075303 homo sapien
2	94	100.0	339	4	Q9UN26 homo sapien
3	94	100.0	339	4	Q9UN25
4	94	100.0	339	4	Q9UN23 homo sapien
5	94	100.0	339	4	Q9UN27
6	94	100.0	339	4	Q9UN27 homo sapien
7	94	100.0	339	4	Q9UN29
8	94	100.0	339	4	Q9UN28 homo sapien
9	94	100.0	339	6	Q9UN28
10	94	100.0	339	6	Q9UN28
11	94	100.0	339	6	Q9UN28
12	94	100.0	339	6	Q9UN29
13	94	100.0	339	6	Q9UN26
14	94	100.0	339	6	Q9UN27
15	94	100.0	339	6	Q9UN27
16	94	100.0	339	6	Q9UN27

Q9tqr2 gorilla gor
Q9tqw5 pan troglod
Q9tnc5 hylobates s
O18771 pan troglod
Q9tnc0 hylobates m
Q9mza3 hylobates a
Q9x899 gorilla gor
Q9un24 homo sapien
Q8hzt9 saimiri sci
Q9tqv7 saguinus sp
Q9tqv7 erythrocebu
Q9tqv6 saguinus sp
Q9tqv6 cercopithec
Q9tut4 macaca neme
Q9tsq1 cercopithec
Q9tut8 cercopithec
Q9tqv7 cercopithec
Q9tut3 macaca mula
Q9tut9 saguinus sp
Q9tut0 macaca fasc
Q9tut9 macaca mula
Q9tsn2 macaca fasc
Q9tut6 cercopithec
Q9tut6 colobus gue
Q9tut6 cercopithec
Q9tsn3 macaca fasc
Q9tut7 macaca fusc
Q9tut2 erythrocebu
Q9tqv0 papio papio
Q9tut6 macaca fusc
Q9tut5 cercopithec
Q9tqv5 saguinus sp
Q9tut7 papio papio
Q9tut5 papio papio
Q9tqv2 papio papio
Q9tqv3 cercopithec
Q9tut8 cercopithec
Q9tut0 saguinus sp
Q9tut3 erythrocebu
Q9tut1 macaca mula
Q9tut2 saguinus sp
Q9tut3 callithrix
Q9tut6 macaca neme
Q9tut1 actus triwi
Q9tqx2 erythrocebu
Q9tut4 mandrillus
Q9tqx3 mandrillus
Q9tut5 alouatta ca
Q9tut5 saguinus sp
Q9tsq4 cercopithec
Q9tut3 macaca neme
Q9tut8 saguinus sp
Q9tut3 saguinus sp
Q9tut8 macaca mula
Q9tut1 macaca neme
Q9tsq3 cercopithec
Q9tut0 cercopithec
Q9tut4 callithrix
Q9tut4 erythrocebu
Q9tut6 erythrocebu
Q9tut2 macaca neme
Q9tut1 macaca mula
Q9tut1 saguinus sp
Q9tut5 macaca neme
Q9tut3 callithrix
Q9tut8 papio papio
Q9tut4 macaca mula
Q9tut6 papio papio
Q9tut7 cercopithec
Q9tut4 cercopithec
Q9tut6 cercopithec
Q9tut0 hylobates c
Q9tsq2 cercopithec

90 90 95.7 339 6 Q9TUR8
 91 90 95.7 339 6 Q9TUV2
 92 90 95.7 339 6 Q9TUV5
 93 90 95.7 339 6 Q9TUV0
 94 90 95.7 339 6 Q9TUR1
 95 90 95.7 339 6 Q9TUS9
 96 90 95.7 340 6 Q9TUV2
 97 90 95.7 344 6 Q9TOR8
 98 90 95.7 352 6 Q9TSK1
 99 90 95.7 352 6 Q9TV48
 100 90 95.7 352 6 Q95NC4

ALIGNMENTS

RESULT 1
 O75303
 ID Q75303 PRELIMINARY; PRT; 215 AA.
 AC O75303;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CC-Chemokine receptor.
 GN CCR-5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tse L., Ehrenberg P.K., Chang G., Michael N.L.;
 RT "Genomic Organization and Functional Characterization of the Complete
 Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-
 Receptor for HIV-1.";
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF009362; AAC21944.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 215 AA; 23946 MW; 3C9146C76BA416F7 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGVGNML 18
 |||||
 DB 33 LPPLYSLVIFGVGNML 50

RESULT 2
 Q9UN26
 ID Q9UN26 PRELIMINARY; PRT; 339 AA.
 AC Q9UN26;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161916; AAD47673.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON TER 1 339
 FT NON TER 339 339
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGVGNML 18
 |||||
 DB 26 LPPLYSLVIFGVGNML 43

RESULT 3
 Q9UN23
 ID Q9UN23 PRELIMINARY; PRT; 339 AA.
 AC Q9UN23;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161920; AAD47677.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON TER 1 339
 FT NON TER 339 339
 SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGVGNML 18
 |||||
 DB 26 LPPLYSLVIFGVGNML 43

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RESULT 4
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korb B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFF1F2F27A CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVFIQFVGNML 18
DB 26 LPPLSLVFIQFVGNML 43

RESULT 5
Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korb B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVFIQFVGNML 18
DB 26 LPPLSLVFIQFVGNML 43

RESULT 6
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korb B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C9FAA7 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVFIQFVGNML 18
DB 26 LPPLSLVFIQFVGNML 43

RESULT 7
Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.

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OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819P92D6DB1A6 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
DB 26 LPPLYSLVIFGFGVGNML 43

RESULT 8
Q9TQW0 ID Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (created gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819P92D6DB1A6 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
DB 26 LPPLYSLVIFGFGVGNML 43

RESULT 9
Q9TUX1 ID Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (created gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB34C4AE CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
DB 26 LPPLYSLVIFGFGVGNML 43

RESULT 10
Q9TUX8 ID Q9TUX8 PRELIMINARY; PRT; 339 AA.
AC Q9TUX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=95959;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
DB 26 LPPLYSLVIFGFGVGNML 43

RESULT 9
Q9TUX1 ID Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (created gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB34C4AE CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
DB 26 LPPLYSLVIFGFGVGNML 43

RESULT 10
Q9TUX8 ID Q9TUX8 PRELIMINARY; PRT; 339 AA.
AC Q9TUX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=95959;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 11
Q9TUN9 PRELIMINARY; PRT; 339 AA.
AC Q9TUN9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161890; AAD47647.1; -.
DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 12
Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
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```
DE C-C chemokine receptor 5 (fragment).
OS CCR5
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161905; AAD47652.1; -.
DR EMBL: AF161898; AAD47655.1; -.
DR EMBL: AF161901; AAD47658.1; -.
DR EMBL: AF161904; AAD47661.1; -.
DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: rhodopsin-like receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 13
Q9TUN6 PRELIMINARY; PRT; 339 AA.
AC Q9TUN6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
OS CCR5
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161900; AAD47657.1; -.
DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
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SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5A4 CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVFIFGVGNML 43

RESULT 14
Q9TUW7
ID Q9TUW7 PRELIMINARY; PRT; 339 AA.
AC Q9TUW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161906; AAD47656.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVFIFGVGNML 43

RESULT 15
Q9TUW3
ID Q9TUW3 PRELIMINARY; PRT; 339 AA.
AC Q9TUW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47664.1; -.
DR EMBL; AF161906; AAD47663.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVFIFGVGNML 43

RESULT 16
Q9TUW2
ID Q9TUW2 PRELIMINARY; PRT; 339 AA.
AC Q9TUW2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47664.1; -.
DR EMBL; AF161906; AAD47663.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39117 MW; 4C4E35825BDS4E9C CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVFIFGVGNML 43

RESULT 17
Q9TOR2
ID Q9TOR2 PRELIMINARY; PRT; 339 AA.
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AC Q9TQR2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161897; AAD47654.1; -
DR EMBL; AF161891; AAD47648.1; -
DR EMBL; AF161892; AAD47649.1; -
DR EMBL; AF161893; AAD47650.1; -
DR EMBL; AF161895; AAD47652.1; -
DR EMBL; AF161896; AAD47653.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39105 MW; F5400A7AB6FF7AB9 CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNNL 18
|||||
Db 26 LPPLYSLVFIQFVGNNL 43

RESULT 18
Q9TQW5
ID Q9TQW5 PRELIMINARY; PRT; 339 AA.
AC Q9TQW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161902; AAD47659.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
SQ SEQUENCE 339 AA; 39105 MW; F5400A7AB6FF7AB9 CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNNL 18
|||||
Db 26 LPPLYSLVFIQFVGNNL 43

RESULT 18
Q9TQW5
ID Q9TQW5 PRELIMINARY; PRT; 339 AA.
AC Q9TQW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161902; AAD47659.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
SQ SEQUENCE 339 AA; 39105 MW; F5400A7AB6FF7AB9 CRC64;

DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39141 MW; DC6E1D627907646C CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNNL 18
|||||
Db 26 LPPLYSLVFIQFVGNNL 43

RESULT 19
Q95NC5
ID Q95NC5 PRELIMINARY; PRT; 352 AA.
AC Q95NC5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177884; AAK43367.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 100.0%; Score 94; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNNL 18
|||||
Db 33 LPPLYSLVFIQFVGNNL 50

RESULT 20
O18771
ID O18771 PRELIMINARY; PRT; 352 AA.
AC O18771;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CCR5 receptor (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHCCR5-141a;
RC

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RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
DR EMBL; AF011539; AAB65739.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 352 AA; 40466 MW; 3FFACTABAEID4FB CRC64;

Query Match 100.0%; Score 94; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
Db |||||
33 LPPLYSLVFIFGVGNML 50

RESULT 21
Q95NCO PRELIMINARY; PRT; 352 AA.
AC Q95NCO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5.
GN CCR5.
OS Hylobates moloch (silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF177899; AAK43382.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 94; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
Db |||||
33 LPPLYSLVFIFGVGNML 50

RESULT 22
Q9MZA3 PRELIMINARY; PRT; 352 AA.
ID Q9MZA3
AC Q9MZA3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Hylobates agilis unko.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9583;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20317091; PubMed=10747879;
RA Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,
RA Begum K., Galvis M.C., Kosteki V., Valente A.J., Murthy K.K.,
RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;
RT "Evolution of human and non-human primate CC chemokine receptor 5 gene
RT and mRNA. Potential roles for haplotype and mRNA diversity,
RT differential haplotype-specific transcriptional activity, and altered
RT transcription factor binding to polymorphic nucleotides in the
RT pathogenesis of HIV-1 and simian immunodeficiency virus.";
RL J. Biol. Chem. 275:18946-18961(2000).
DR EMBL; AF252551; AAF87981.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40293 MW; BAF8279ABBAB5309 CRC64;

Query Match 100.0%; Score 94; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
Db |||||
33 LPPLYSLVFIFGVGNML 50

RESULT 23
Q9XS99 PRELIMINARY; PRT; 352 AA.
AC Q9XS99;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CC chemokine receptor 5.
GN CCR5.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GorillaCCR;
RX MEDLINE=99210133; PubMed=10195758;
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
RT nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
DR EMBL; AF105291; AAD20560.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

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```
KW Receptor.
SQ SEQUENCE 352 AA; 40529 MW; 1BE68C68FE2E7AD0 CRC64;

Query Match 100.0%; Score 94; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 33 LPPLYSLVIFGFVGNML 50

RESULT 24
Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD47676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; R:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 97.9%; Score 92; DB 4; Length 339;
Best Local Similarity 94.4%; Pred. No. 2.5e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVIFGFVGNML 43

RESULT 25
Q8H2T9 PRELIMINARY; PRT; 352 AA.
AC Q8H2T9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine receptor CCR5.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RA LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT "Blockade of HIV-1 infection of New World Monkey Cells Occurs
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RT Primarily at the Stage of Virus Entry.";
RL J. Exp. Med. 196;431-445(2002).
DR EMBL; AF452615; AAI14531.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40542 MW; 9FC896FB7F074647 CRC64;

Query Match 97.9%; Score 92; DB 6; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.6e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 33 LPPLYSLVIFGFVGNML 50

RESULT 26
Q9TUV7 PRELIMINARY; PRT; 316 AA.
AC Q9TUV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161930; AAD47687.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 316
SQ SEQUENCE 316 AA; 36517 MW; 4DAD95C3848F04EA CRC64;

Query Match 95.7%; Score 90; DB 6; Length 316;
Best Local Similarity 88.9%; Pred. No. 4.9e-06;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LPPLYSLVFIFGVGNML 18
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Db 3 LPPLYSNVLFGFVGNML 20

RESULT 27
Q9TUQ7 PRELIMINARY; PRT; 334 AA.
AC Q9TUQ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Brythocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Brythocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162049; AAD47804.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 334
SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 95.7%; Score 90; DB 6; Length 334;
Best Local Similarity 94.4%; Pred. No. 5.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
  |||||:|||||
Db 21 LPPLYSLVFIFGVGNIL 38

RESULT 28
Q9TUV6 PRELIMINARY; PRT; 339 AA.
AC Q9TUV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161932; AAD47689.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.

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DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 38993 MW; 0559F4F0FEC70F5F CRC64;

Query Match 95.7%; Score 90; DB 6; Length 339;
Best Local Similarity 88.9%; Pred. No. 5.2e-06;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
  |||||:|||||
Db 26 LPPLYSNVLFGFVGNML 43

RESULT 29
Q9TUU9 PRELIMINARY; PRT; 339 AA.
AC Q9TUU9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161948; AAD47704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 95.7%; Score 90; DB 6; Length 339;
Best Local Similarity 94.4%; Pred. No. 5.2e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
  |||||:|||||
Db 26 LPPLYSLVFIFGVGNIL 43

RESULT 30
Q9TUT4

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ID O9TUT4 PRELIMINARY; PERT; 339 AA.
AC O9TUT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shabara R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; RAD47734.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match 95.7%; Score 90; DB 6; Length 339;
Best Local Similarity 94.4%; Pred. NO. 5.2e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
Db |||||:|||||:|
26 LPPLYSLVFIFGVGNIL 43

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Search completed: March 4, 2004, 18:02:54
 Job time : 31.0204 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:55:22 ; Search time 11.5714 Seconds
(without alignments)
80.307 Million cell updates/sec

Title: US-10-084-813-11
Perfect score: 94
Sequence: 1 LPPLYSIVFIQFVGNML 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	83	4	US-09-131-827A-13
2	94	100.0	87	3	US-09-087-232A-18
3	94	100.0	100	3	US-09-087-232A-15
4	94	100.0	184	4	US-08-833-752-4
5	94	100.0	215	3	US-09-087-232A-17
6	94	100.0	215	4	US-08-833-752-6
7	94	100.0	329	4	US-09-502-783A-9
8	94	100.0	344	3	US-08-466-343D-9
9	94	100.0	347	1	US-08-461-244-3
10	94	100.0	352	3	US-08-466-343D-2
11	94	100.0	352	3	US-09-087-232A-13
12	94	100.0	352	3	US-08-861-105-14
13	94	100.0	352	3	US-08-575-967A-2
14	94	100.0	352	3	US-09-045-583-52
15	94	100.0	352	4	US-09-517-605-5
16	94	100.0	352	4	US-09-833-752-5
17	94	100.0	352	4	US-08-833-752-5
18	94	100.0	352	4	US-09-502-783A-2
19	94	100.0	352	4	US-09-796-202-1
20	94	100.0	360	1	US-08-450-393A-4
21	94	100.0	360	3	US-08-446-669-4
22	94	100.0	360	3	US-09-045-583-50
23	94	100.0	360	3	US-09-045-583-51
24	94	100.0	360	4	US-09-534-185-50
25	94	100.0	360	4	US-09-534-185-51
26	94	100.0	360	4	US-08-833-752-7
27	94	100.0	360	4	US-09-131-827A-2

28	94	100.0	360	4	US-09-131-827A-20	Sequence 20, Appl
29	94	100.0	360	5	PCT-US95-00476-4	Sequence 4, Appl
30	94	100.0	374	1	US-08-450-393A-2	Sequence 2, Appl
31	94	100.0	374	3	US-08-446-669-2	Sequence 2, Appl
32	94	100.0	374	5	PCT-US95-00476-2	Sequence 2, Appl
33	88	93.6	354	4	US-08-724-984A-2	Sequence 2, Appl
34	77	81.9	355	1	US-08-012-988A-2	Sequence 2, Appl
35	77	81.9	355	1	US-08-450-393A-5	Sequence 5, Appl
36	77	81.9	355	3	US-08-446-669-5	Sequence 5, Appl
37	77	81.9	355	3	US-09-045-583-53	Sequence 53, Appl
38	77	81.9	355	4	US-09-239-938-1	Sequence 1, Appl
39	77	81.9	355	4	US-09-534-185-53	Sequence 53, Appl
40	77	81.9	355	4	US-08-833-752-9	Sequence 9, Appl
41	77	81.9	355	4	US-09-886-319A-13	Sequence 13, Appl
42	77	81.9	355	4	US-09-886-319A-14	Sequence 14, Appl
43	77	81.9	355	5	PCT-US95-00476-5	Sequence 5, Appl
44	75	79.8	360	3	US-08-875-573-20	Sequence 20, Appl
45	75	79.8	360	3	US-09-232-878-2	Sequence 2, Appl
46	75	79.8	360	3	US-09-045-583-55	Sequence 55, Appl
47	75	79.8	360	4	US-09-534-185-55	Sequence 55, Appl
48	70	74.5	360	4	US-08-939-107-34	Sequence 34, Appl
49	70	74.5	355	4	US-08-720-585-2	Sequence 2, Appl
50	68	72.3	360	4	US-08-833-752-10	Sequence 10, Appl
51	65	69.1	355	4	US-08-833-752-8	Sequence 8, Appl
52	63	67.0	355	3	US-08-575-967A-4	Sequence 4, Appl
53	63	67.0	355	3	US-08-847-296B-1	Sequence 1, Appl
54	63	67.0	355	3	US-09-045-583-54	Sequence 54, Appl
55	63	67.0	355	4	US-09-534-185-54	Sequence 54, Appl
56	63	67.0	355	4	US-08-720-585-4	Sequence 4, Appl
57	63	67.0	355	4	US-08-720-585-6	Sequence 6, Appl
58	63	67.0	356	4	US-08-567-882-7	Sequence 7, Appl
59	63	67.0	357	4	US-09-266-464-2	Sequence 2, Appl
60	63	67.0	357	4	US-09-170-496D-24	Sequence 24, Appl
61	63	67.0	357	4	US-09-170-496D-176	Sequence 176, App
62	61	64.9	378	3	US-09-045-583-5	Sequence 5, Appl
63	61	64.9	378	4	US-09-534-185-5	Sequence 5, Appl
64	60	63.8	107	4	US-09-621-976-5333	Sequence 5333, Ap
65	60	63.8	348	3	US-08-852-824-17	Sequence 17, Appl
66	60	63.8	352	1	US-08-450-393A-6	Sequence 6, Appl
67	60	63.8	352	3	US-08-446-669-6	Sequence 6, Appl
68	60	63.8	352	5	PCT-US95-00476-6	Sequence 6, Appl
69	60	63.8	361	1	US-08-383-750-4	Sequence 4, Appl
70	60	63.8	361	3	US-08-352-678-4	Sequence 4, Appl
71	60	63.8	361	4	US-09-536-954-4	Sequence 4, Appl
72	60	63.8	361	4	US-09-170-496D-78	Sequence 78, Appl
73	60	63.8	361	4	US-09-170-496D-206	Sequence 206, App
74	60	63.8	361	5	PCT-US93-0936-4	Sequence 4, Appl
75	59	62.8	373	3	US-08-559-524A-4	Sequence 4, Appl
76	59	62.8	373	3	US-08-749-707-4	Sequence 4, Appl
77	59	62.8	373	4	US-09-947-922-4	Sequence 2, Appl
78	58	61.7	384	3	US-09-045-583-2	Sequence 2, Appl
79	58	61.7	384	4	US-09-534-185-2	Sequence 2, Appl
80	57	60.6	337	1	US-08-153-848-46	Sequence 46, Appl
81	57	60.6	337	3	US-09-239-843A-46	Sequence 46, Appl
82	57	60.6	337	4	US-09-088-337B-46	Sequence 46, Appl
83	57	60.6	337	5	PCT-US93-11153-46	Sequence 46, Appl
84	57	60.6	352	1	US-08-203-056-3	Sequence 3, Appl
85	57	60.6	352	1	US-08-076-093A-4	Sequence 4, Appl
86	57	60.6	352	1	US-08-701-265-4	Sequence 4, Appl
87	57	60.6	352	2	US-08-284-586-4	Sequence 4, Appl
88	57	60.6	352	2	US-08-805-478-4	Sequence 4, Appl
89	57	60.6	352	2	US-08-802-627A-4	Sequence 4, Appl
90	57	60.6	352	2	US-08-801-238-4	Sequence 4, Appl
91	57	60.6	352	2	US-08-801-228-4	Sequence 4, Appl
92	57	60.6	352	3	US-09-104-296-4	Sequence 4, Appl
93	57	60.6	352	4	US-09-517-605-4	Sequence 4, Appl
94	57	60.6	362	3	US-08-513-974B-374	Sequence 374, App
95	57	60.6	368	3	US-08-709-838-2	Sequence 2, Appl
96	57	60.6	368	3	US-08-829-839-2	Sequence 2, Appl
97	57	60.6	368	4	US-09-170-496D-20	Sequence 20, Appl
98	57	60.6	368	4	US-09-170-496D-174	Sequence 174, App
99	57	60.6	368	4	US-09-624-594-2	Sequence 2, Appl
100	56	59.6	325	1	US-08-118-270-51	Sequence 51, Appl

TELEFAX: (212) 765-2519

; Patent No: 6448375

```

/ ATTORNEY/AGENT INFORMATION:
/ NAME: KOLE, LISA B.
/ REGISTRATION NUMBER: 35,225
/ REFERENCE/DOCKET NUMBER: AP 31115
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 408-2628
/ TELEFAX: (212) 765-2519
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-087-232A-17

Query Match 100.0%; Score 94; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYLSLVFIQFGVGNML 18
Db 33 LPPYLSLVFIQFGVGNML 50

RESULT 6
US-08-833-752-6
/ Sequence 6, Application US/08833752
/ Patent No. 6448375
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92860
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/833,752
/ FILING DATE: 9-APR-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER:
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-833-752-6

Query Match 100.0%; Score 94; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYLSLVFIQFGVGNML 18
Db 33 LPPYLSLVFIQFGVGNML 50

```

RESULT 7

US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. 651826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CGR)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match 100.0%; Score 94; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
|||
DB 28 LPPLYSLVFIFGFVGNML 45

RESULT 8

US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; REGISTRATION NUMBER: 36,134
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-9

Query Match 100.0%; Score 94; DB 3; Length 344;

Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
|||
DB 28 LPPLYSLVFIFGFVGNML 45

RESULT 9

US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-3

Query Match 100.0%; Score 94; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
|||
DB 32 LPPLYSLVFIFGFVGNML 49

RESULT 10

US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 100.0%; Score 94; DB 3; Length 344;

;; CITY: WASHINGTON
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;;
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/466,343D
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEFFE, ERIC K.
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-466-343D-2

Query Match 100.0%; Score 94; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLXSLVFIFGFVGNML 18
Db 33 LPPLXSLVFIFGFVGNML 50

RESULT 11
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANT ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, Lisa B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-087-232A-13

Query Match 100.0%; Score 94; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLXSLVFIFGFVGNML 18
Db 33 LPPLXSLVFIFGFVGNML 50

RESULT 12
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; TITLE OF INVENTION: USRS THEREOF
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-861-105-14

Query Match 100.0%; Score 94; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
Db 33 LPPLYSLVIFGVGNML 50

RESULT 13
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"

US-08-575-967A-2

Query Match 100.0%; Score 94; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
Db 33 LPPLYSLVIFGVGNML 50

RESULT 14
US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts

; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-52

Query Match 100.0%; Score 94; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
Db 33 LPPLYSLVIFGVGNML 50

RESULT 15
US-09-517-605-5
; Sequence 5, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
; APPLICANT: Littman, Dan R.
; APPLICANT: Kwon, Douglas S.
; APPLICANT: van Kooyk, Yvette
; APPLICANT: Geijtenbeek, Theo
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
; FILE REFERENCE: 1049-1-017
; CURRENT APPLICATION NUMBER: US/09/517,605
; CURRENT FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-517-605-5

Query Match 100.0%; Score 94; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
Db 33 LPPLYSLVIFGVGNML 50

RESULT 16
US-09-534-185-52
; Sequence 52, Application US/09534185

Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Hepathelical Receptor Superfamily and Uses
thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52
Query Match 100.0%; Score 94; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPPLYSLVFIQFVGNNL 18
Db 33 LPPLYSLVFIQFVGNNL 50
RESULT 17
US-08-833-752-5
Sequence 5, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-5
Query Match 100.0%; Score 94; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPPLYSLVFIQFVGNNL 18
Db 33 LPPLYSLVFIQFVGNNL 50
RESULT 18
US-09-502-783A-2
Sequence 2, Application US/09502783A
Patent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CKR5
FILE REFERENCE: HDGNN10
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2
Query Match 100.0%; Score 94; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPPLYSLVFIQFVGNNL 18
Db 33 LPPLYSLVFIQFVGNNL 50
RESULT 19
US-09-796-202-1
Sequence 1, Application US/09796202
Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CKR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 1

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; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match      100.0%; Score 94; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLYSLVIFGFGVGNML 18
Db      33 LPPLYSLVIFGFGVGNML 50

RESULT 20
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMAOTTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: May 25, 1995
; APPLICATION NUMBER: US/08/450,393A
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-4

Query Match      100.0%; Score 94; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLYSLVIFGFGVGNML 18
Db      45 LPPLYSLVIFGFGVGNML 62

RESULT 21
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMAOTTRACTANT
```

```
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4

Query Match      100.0%; Score 94; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLYSLVIFGFGVGNML 18
Db      45 LPPLYSLVIFGFGVGNML 62

RESULT 22
US-09-045-583-50
; Sequence 50, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
```


REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-50

Query Match 100.0%; Score 94; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVPIFGVGNML 18
|||||
DB 45 LPPLYSLVPIFGVGNML 62

RESULT 23

US-09-045-583-51
Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 5287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-51

Query Match 100.0%; Score 94; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVPIFGVGNML 18
|||||
DB 45 LPPLYSLVPIFGVGNML 62

RESULT 24

US-09-534-185-50
Sequence 50, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match 100.0%; Score 94; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVPIFGVGNML 18
|||||
DB 45 LPPLYSLVPIFGVGNML 62

RESULT 25

US-09-534-185-51
Sequence 51, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

Query Match 100.0%; Score 94; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
|||||
Db 45 LPPLYSLVIFGFGVGNML 62

RESULT 26
US-08-833-752-7
Sequence 7, Application US/08833752
Patent No. 6448375
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6448375e
US-08-833-752-7

Query Match 100.0%; Score 94; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
|||||
Db 45 LPPLYSLVIFGFGVGNML 62

RESULT 27
US-09-131-827A-2
Sequence 2, Application US/09131827A
Patent No. 6600030
GENERAL INFORMATION:
APPLICANT: Dean, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
FILE REFERENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 100.0%; Score 94; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
|||||
Db 45 LPPLYSLVIFGFGVGNML 62

RESULT 28
US-09-131-827A-20
Sequence 20, Application US/09131827A
Patent No. 6600030
GENERAL INFORMATION:
APPLICANT: Dean, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
FILE REFERENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/055,659
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-131-827A-20

Query Match 100.0%; Score 94; DB 4; Length 360;

Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNML 18
Db 45 LPPLYSLVFIQFVGNML 62

RESULT 29

PCT-US95-00476-4

; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA

; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US95-00476-4

Query Match 100.0%; Score 94; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNML 18
Db 45 LPPLYSLVFIQFVGNML 62

RESULT 30

US-08-450-393A-2

; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA

; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEVPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-450-393A-2

Query Match 100.0%; Score 94; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. NO. 3.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNML 18
Db 45 LPPLYSLVFIQFVGNML 62

Search completed: March 4, 2004, 18:05:12
Job time : 12.5714 secs

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	94	100.0	18	14	US-10-084-813-11	Sequence 11, Appl
2	94	100.0	18	14	US-10-084-813-39	Sequence 39, Appl
3	94	100.0	83	9	US-09-131-827A-13	Sequence 13, Appl
4	94	100.0	184	9	US-09-938-719-4	Sequence 4, Appl
5	94	100.0	184	9	US-09-939-226-4	Sequence 4, Appl
6	94	100.0	184	9	US-09-938-703-4	Sequence 4, Appl
7	94	100.0	215	9	US-09-938-719-6	Sequence 6, Appl
8	94	100.0	215	9	US-09-939-226-6	Sequence 6, Appl
9	94	100.0	215	9	US-09-938-703-6	Sequence 6, Appl
10	94	100.0	329	9	US-09-735-285-9	Sequence 9, Appl
11	94	100.0	329	9	US-09-135-662A-9	Sequence 9, Appl
12	94	100.0	329	9	US-09-339-912A-9	Sequence 9, Appl
13	94	100.0	329	9	US-09-502-783A-9	Sequence 9, Appl
14	94	100.0	332	14	US-10-095-876A-2	Sequence 2, Appl
15	94	100.0	344	9	US-09-779-879A-9	Sequence 9, Appl

89 75 79.8 360 14 US-10-164-649-55 Sequence 55, Appl
90 75 79.8 360 14 US-10-231-452-48 Sequence 48, Appl
91 75 79.8 360 14 US-10-239-423-66 Sequence 66, Appl
92 73 77.7 18 14 US-10-084-813-38 Sequence 38, Appl
93 72 76.6 18 14 US-10-084-813-40 Sequence 40, Appl
94 70 74.5 355 14 US-10-283-028-2 Sequence 2, Appl
95 68 72.3 360 9 US-09-938-719-10 Sequence 10, Appl
96 68 72.3 360 9 US-09-939-226-10 Sequence 10, Appl
97 68 72.3 360 9 US-09-938-703-10 Sequence 8, Appl
98 65 69.1 355 9 US-09-938-719-8 Sequence 8, Appl
99 65 69.1 355 9 US-09-939-226-8 Sequence 8, Appl
100 65 69.1 355 9 US-09-938-703-8

ALIGNMENTS

RESULT 1
US-10-084-813-11
; Sequence 11, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-11

Query Match 100.0%; Score 94; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNML 18
Db 1 LPPLYSLVFIQFVGNML 18

RESULT 2
US-10-084-813-39
; Sequence 39, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-39

Query Match 100.0%; Score 94; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNML 18
Db 1 LPPLYSLVFIQFVGNML 18

RESULT 3
US-09-131-827A-13
; Sequence 13, Application US/09131827A
; Patent No. US20020038469A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-13

Query Match 100.0%; Score 94; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNML 18
Db 45 LPPLYSLVFIQFVGNML 62

RESULT 4
US-09-938-719-4
; Sequence 4, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4

Query Match 100.0%; Score 94; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIQFGVGNML 18
Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 5
US-09-939-226-4
Sequence 4, Application US/09939226
Patent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4

Query Match 100.0%; Score 94; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIQFGVGNML 18
Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 6
US-09-938-703-4
Sequence 4, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

Query Match 100.0%; Score 94; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIQFGVGNML 18
Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 7
US-09-938-719-6
Sequence 6, Application US/09938719
Patent No. US20020106742A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4

Query Match 100.0%; Score 94; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIQFGVGNML 18
Db 33 LPPLYSLVFIQFGVGNML 50

Qy 1 LPPLYSLVFIQFGVGNML 18
Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 6
US-09-938-703-4
Sequence 4, Application US/09938703
Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-703-4

Query Match 100.0%; Score 94; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIQFGVGNML 18
Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 7
US-09-938-719-6
Sequence 6, Application US/09938719
Patent No. US20020106742A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-939-226-4

Query Match 100.0%; Score 94; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIQFGVGNML 18
Db 33 LPPLYSLVFIQFGVGNML 50

/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/938,719
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 27-JULY-2000
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6
Query Match 100.0%; Score 94; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPPLYSLVFIFGFVGNML 18
DB 33 LPPLYSLVFIFGFVGNML 50
RESULT 8
US-09-939-226-6
/ Sequence 6, Application US/09939226
/ Patent No. US20020110805A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ PARMENTIER, MARC
/ VASSART, GILBERT
/ LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/939,226
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 2000-07-27
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6

/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6
Query Match 100.0%; Score 94; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPPLYSLVFIFGFVGNML 18
DB 33 LPPLYSLVFIFGFVGNML 50
RESULT 9
US-09-938-703-6
/ Sequence 6, Application US/09938703
/ Patent No. US20020110870A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ PARMENTIER, MARC
/ VASSART, GILBERT
/ LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/938,703
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 2000-07-27
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6
Query Match 100.0%; Score 94; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPPLYSLVFIFGFVGNML 18
DB 33 LPPLYSLVFIFGFVGNML 50
RESULT 10
US-09-725-285-9

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; Sequence 9, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-725-285-9

Query Match      100.0%; Score 94; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLYSLVFIFGFGVGNML 18
      |||||
DB      28 LPPLYSLVFIFGFGVGNML 45

RESULT 11
US-09-195-662A-9
; Sequence 9, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-195-662A-9

Query Match      100.0%; Score 94; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLYSLVFIFGFGVGNML 18
      |||||
DB      28 LPPLYSLVFIFGFGVGNML 45

RESULT 12
US-09-339-912A-9
; Sequence 9, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; FILE REFERENCE: 1488.1150003
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; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-339-912A-9

Query Match      100.0%; Score 94; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLYSLVFIFGFGVGNML 18
      |||||
DB      28 LPPLYSLVFIFGFGVGNML 45

RESULT 13
US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. US20020132269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match      100.0%; Score 94; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLYSLVFIFGFGVGNML 18
      |||||
DB      28 LPPLYSLVFIFGFGVGNML 45

RESULT 14
US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030148294A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Bandman, Olga
; APPLICANT: Coleman, Roger; Wilde, Craig G.
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
; FILE REFERENCE: PF-0060-1 CON
; CURRENT APPLICATION NUMBER: US/10/095,876A
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 08/638,081
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

Query Match 100.0%; Score 94; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPELYSLVFIFGVGNML 18
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Db 24 LPELYSLVFIFGVGNML 41

RESULT 15

US-09-779-879A-9
Sequence 9, Application US/09779879A
Patent No. US20020048786A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000A
CURRENT APPLICATION NUMBER: US/09/779,879A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/234,336
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-879A-9

Query Match 100.0%; Score 94; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPELYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 28 LPELYSLVFIFGVGNML 45

RESULT 16

US-09-779-880A-9
Sequence 9, Application US/09779880A
Patent No. US20020061834A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Roschke, Viktor
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000C
CURRENT APPLICATION NUMBER: US/09/779,880A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,258
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 60/187,999
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/234,336
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-880A-9

TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-880A-9

Query Match 100.0%; Score 94; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPELYSLVFIFGVGNML 18
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Db 28 LPELYSLVFIFGVGNML 45

RESULT 17

US-10-232-686-9
Sequence 9, Application US/10232686
Publication No. US20030023044A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000N
CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 9
LENGTH: 344
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-232-686-9

Query Match 100.0%; Score 94; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPELYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 28 LPELYSLVFIFGVGNML 45

RESULT 18

US-10-067-800-9
Sequence 9, Application US/10067800
Publication No. US20030100058A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000I
CURRENT APPLICATION NUMBER: US/10/067,800
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: PCT/US01/04153
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/779,880
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/297,257
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/310,458
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/328,447
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/341,725
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin version 3.1
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-067-800-9

; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-9

Query Match 100.0%; Score 94; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
Db 28 LPPLYSLVFIFGVGNML 45

RESULT 19

US-10-135-839-9
; Sequence 9, Application US/10135839
; Publication No. US20030166024A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/10/135,839
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-135-839-9

Query Match 100.0%; Score 94; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
Db 28 LPPLYSLVFIFGVGNML 45

RESULT 20

US-09-104-792-3
; Sequence 3, Application US/09104792
; Patent No. US20020019026A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/176,078
; FILING DATE: 21-Jun-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,792
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-104-792-3

Query Match 100.0%; Score 94; DB 9; Length 347;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
Db 32 LPPLYSLVFIFGVGNML 49

RESULT 21

US-10-176-078-3
; Sequence 3, Application US/10176078
; Publication No. US20030165901A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/176,078
; FILING DATE: 21-Jun-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid

;
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-176-078-3

Query Match 100.0%; Score 94; DB 14; Length 347;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
|||
Db 32 LPPLYSLVVFIFGVGNML 49

RESULT 22
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 94; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
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Db 33 LPPLYSLVVFIFGVGNML 50

RESULT 23
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manousos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

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; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 100.0%; Score 94; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
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Db 33 LPPLYSLVVFIFGVGNML 50

RESULT 24
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-2

Query Match 100.0%; Score 94; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
|||
Db 33 LPPLYSLVVFIFGVGNML 50

RESULT 25
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352

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/ ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match      100.0%; Score 94; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPELSLVFIQFVGNNML 18
   |||||
DB 33 LPELSLVFIQFVGNNML 50

RESULT 28
US-09-813-653-15
/ Sequence 15, Application US/09813653
/ Patent No. US20020064770A1
/ GENERAL INFORMATION:
/ APPLICANT: Nestor, John
/ APPLICANT: Wilson, Carol
/ APPLICANT: See, Raymond
/ APPLICANT: Tan Hehir, Christina
/ TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
/ FILE REFERENCE: CNS-005
/ CURRENT APPLICATION NUMBER: US/09/813,653
/ CURRENT FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: US 60/190,946
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/190,996
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/191,299
/ PRIOR FILING DATE: 2000-03-21
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 15
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-813-653-15

Query Match      100.0%; Score 94; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPELSLVFIQFVGNNML 18
   |||||
DB 33 LPELSLVFIQFVGNNML 50

RESULT 29
US-09-813-653-17
/ Sequence 17, Application US/09813653
/ Patent No. US20020064770A1
/ GENERAL INFORMATION:
/ APPLICANT: Nestor, John
/ APPLICANT: Wilson, Carol
/ APPLICANT: See, Raymond
/ APPLICANT: Tan Hehir, Christina
/ TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
/ FILE REFERENCE: CNS-005
/ CURRENT APPLICATION NUMBER: US/09/813,653
/ CURRENT FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: US 60/190,946
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/190,996
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: US 60/191,299
/ PRIOR FILING DATE: 2000-03-21
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: Patent in version 3.0
/ SEQ ID NO 17
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens

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US-09-813-653-17

Query Match 100.0%; Score 94; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIKFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
DB 33 LPPLYSLVFIKFGVGNML 50

RESULT 30

US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US2002006813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 94; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIKFGVGNML 18
| | | | | | | | | | | | | | | | | | | | | |
DB 33 LPPLYSLVFIKFGVGNML 50

Search completed: March 4, 2004, 18:22:51
Job time : 25.0612 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 52.3061 Seconds
(without alignments)
118.840 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNTMQLLTGLYFIFGFFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	22	4	AAB88994
2	126	100.0	184	2	AAW27406
3	126	100.0	215	2	AAW27408
4	126	100.0	215	2	AAW88238
5	126	100.0	268	7	ADC10142
6	126	100.0	268	7	ADC10144
7	126	100.0	332	2	AAW26766
8	126	100.0	352	2	AAW27407
9	126	100.0	352	2	AAW27123
10	126	100.0	352	2	AAW27125
11	126	100.0	352	2	AAW07602
12	126	100.0	352	2	AAW23835
13	126	100.0	352	2	AAW88232
14	126	100.0	352	3	AAW80128
15	126	100.0	352	4	AAW79089
16	126	100.0	352	4	AAW07046
17	126	100.0	352	4	AAW07048
18	126	100.0	352	4	AAW80111
19	126	100.0	352	4	AAW04321
20	126	100.0	352	4	AAW07037
21	126	100.0	352	4	AAW07039
22	126	100.0	352	4	AAW46858
23	126	100.0	352	4	AAW56342
24	126	100.0	352	4	AAW83354
25	126	100.0	352	4	AAW82948

26	126	100.0	352	5	AAU97150
27	126	100.0	352	5	AAU97152
28	126	100.0	352	5	AAW52829
29	126	100.0	352	5	AAW52828
30	126	100.0	352	5	ABG70597
31	126	100.0	352	5	ABG92883
32	126	100.0	352	5	ABG92880
33	126	100.0	352	5	AAE25808
34	126	100.0	352	5	AAE25811
35	126	100.0	352	5	ABE81054
36	126	100.0	352	5	ABE808343
37	126	100.0	352	6	ABG75540
38	126	100.0	352	6	ABR58602
39	126	100.0	352	6	AAU29514
40	126	100.0	352	6	AAU61654
41	126	100.0	352	6	ABP97728
42	126	100.0	352	6	ABP81933
43	126	100.0	352	7	ADC03341
44	126	100.0	352	7	ADC03359
45	126	100.0	371	2	AAW23834
46	126	100.0	439	2	AAV41280
47	104	82.5	18	4	ABE88931
48	98	77.8	18	4	ABE88932
49	87	69.0	344	5	ABG92881
50	87	69.0	344	6	ABU61655
51	87	69.0	360	2	AAW79166
52	87	69.0	360	2	AAW35833
53	87	69.0	360	4	AAW80108
54	87	69.0	360	4	AAU07613
55	87	69.0	360	4	AAU07614
56	87	69.0	360	4	ABE56340
57	87	69.0	360	6	ABP97725
58	87	69.0	360	6	ABP81987
59	87	69.0	374	2	AAW79165
60	87	69.0	374	4	AAW80107
61	87	69.0	374	6	AAU09083
62	87	69.0	374	7	ADD44861
63	87	69.0	374	7	ADD44865
64	84	66.7	354	7	ADD44859
65	84	66.7	354	7	ADD44863
66	83	65.9	18	4	ABE88930
67	83	65.9	269	2	AAW26429
68	83	65.9	269	4	AAW68250
69	82	65.1	355	2	AAW07618
70	82	65.1	355	2	AAW49807
71	82	65.1	355	2	AAW56689
72	82	65.1	355	2	AAW97868
73	82	65.1	355	4	ABE80115
74	82	65.1	355	4	ABE56343
75	82	65.1	355	5	AAU80223
76	82	65.1	355	5	AAU80222
77	82	65.1	355	5	AAU77932
78	82	65.1	355	6	ABP97731
79	82	65.1	355	6	ABP81794
80	82	65.1	358	5	AAU77933
81	82	63.5	354	2	AAW54037
82	76	60.3	18	4	ABE88933
83	76	60.3	355	2	AAW29179
84	76	60.3	355	7	ADD45360
85	74	58.7	329	4	AAW23921
86	74	58.7	329	4	AAW46859
87	74	58.7	329	5	ABE81055
88	74	58.7	356	5	AAO22920
89	71	56.3	295	4	AAW80106
90	71	56.3	355	2	AAE52749
91	71	56.3	355	2	AAW25751
92	71	56.3	355	2	AAW26588
93	71	56.3	355	3	AAE20571
94	71	56.3	355	6	ABU09082
95	71	56.3	355	6	ABP97724
96	71	56.3	355	6	ABP81790
97	67	53.2	332	5	ABJ03698
98	67	53.2	355	2	AAW03376

AAU97150	Human G-p
AAU97152	Human G-p
AAW52829	Human CCR
AAW52828	Human CC
ABG70597	Human G-p
ABG92883	Human Imm
ABG92880	Human G-p
AAE25808	Human G-p
AAE25811	Human G-p
ABE81054	G-protein
ABE808343	Human che
ABG75540	Human G-p
ABR58602	Human can
AAU29514	Human C-C
AAU61654	Human G-p
ABP97728	Amino aci
ABP81933	Human C-C
ADC03341	Human che
ADC03359	Macaque c
AAW23834	Human CC
AAV41280	Fusion pr
ABE88931	HIV gp120
ABE88932	HIV gp120
ABG92881	Class I r
ABU61655	Human mon
AAW79166	Human mon
AAW35833	Human mon
AAW80108	Human CCR
AAU07613	Human CCR
AAU07614	Human wll
ABE56340	Non-endog
ABP97725	Amino aci
ABP81987	Human C-C
AAW79165	Human mon
AAW80107	Human CCR
AAU09083	Human che
ADD44861	Human Pro
ADD44865	Human Pro
ADD44859	Rat Prote
ADD44863	Rat Prote
ABE88930	HIV gp120
AAW26429	Swinepox
AAW68250	Protein e
AAW07618	Human G-p
AAW49807	Human G-p
AAW56689	Human MCP
AAW97868	Human CC
ABE80115	Human CCR
ABE56343	Non-endog
AAU80223	Human Che
AAU80222	Human Che
AAU77932	Human G-p
ABP97731	Amino aci
ABP81794	Human C-C
AAU77933	Human G-p
AAW54037	Mouse CC
AAW29179	Rat CC ch
AAW23921	68 aa G-p
AAW46859	Human MCP
ABE81055	Human MCP
AAO22920	356 aa G-
AAW80106	Human CCR
AAE52749	C-C chemo
AAW25751	Human XIP
AAW26588	Human XIP
AAE20571	Human CC-
ABU09082	Human che
ABP97724	Amino aci
ABP81790	Human C-C
ABJ03698	Human ova
AAW03376	CC-chemok

99 67 53.2 355 2 AAW03377 CC-chemok
100 67 53.2 355 2 AAW03378 CC-chemok

ALIGNMENTS

RESULT 1

AA088994
ID AAB88994 standard; peptide; 22 AA.

XX AC AAB88994;

XX DT 23-MAY-2001 (first entry)

XX DE HIV gp120 protein binding peptide #87.

XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.

XX OS Homo sapiens.

XX PN WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US023505.

XX PR 27-AUG-1999; 99US-0151270P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Saxinger C;

XX DR WPI; 2001-244398/25.

XX PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.

XX PS Claim 21; Page 38; 114pp; English.

XX CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention

XX SQ Sequence 22 AA;

Query Match 100.0%; Score 126; DB 4; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.2e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22

DB 1 QWDFGNTMCQLLTGLYFIGFFS 22

RESULT 2

AAW27406

ID AAW27406 standard; protein; 184 AA.

XX AC AAW27406;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;

XX KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;

XX KW predisposition; resistance; diagnosis; treatment; prevention;

XX KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;

KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW atherosclerosis; autoimmune disorder.

OS Homo sapiens.

XX WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX PA (EURO-) EUROSCREEN SA.

XX FI Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

XX DR N-PSDB; AAT90116.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
PT disease and viral infection.

XX PS Claim 1; Fig 1a; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
CC '5 (CCRs), which is not a receptor of human immunodeficiency virus type 1
CC or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat
CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
CC viral infections, especially HIV-1 or HIV-2 infection, cancer,
CC atherosclerosis and autoimmune disorders. Subjects that express the
CC inactive receptor have a predisposition, or resistance to HIV-1 and/or
CC HIV-2

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 126; DB 2; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.2e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22

DB 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 3

AAW27408

ID AAW27408 standard; protein; 215 AA.

XX AC AAW27408;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;
XX KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
XX KW predisposition; resistance; diagnosis; treatment; prevention;
XX KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
XX KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
XX KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX PN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

Fri Mar 5 14:59:12 2004

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PR 01-MAR-1996; 96EP-00870021.
PR 06-AUG-1996; 96EP-00870102.
XX (EURO-) EUROSCREEN SA.
XX Samson M, Parmentier M, Vassart G, Libert F;
PI WPI; 1997-479829/44.
XX N-PSDB; AAT90118.
DR Active and inactive forms of human CC chemokine receptor CCR-5 - useful
XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
XX disease and viral infection.
XX Claim 7; Fig id-e; 94pp; English.
XX The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
XX 5 (CCR5), which lacks the last 3 transmembrane regions and the regions
XX involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,
XX treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
XX glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
XX viral infections, especially human immunodeficiency virus type 1 or type
XX 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune
XX disorders. Subjects that express the inactive receptor have a
XX predisposition, or resistance to HIV-1 and/or HIV-2
XX
XX Sequence 215 AA;
Query Match 100.0%; Score 126; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 4
AAW88238
ID AAW88238 standard; protein; 215 AA.
XX AAW88238;
XX
XX 15-MAR-1999 (first entry)
XX HIV-1 co-receptor CCR5 variant CCR5-delta32.
XX HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
XX gene therapy; human.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain 32..56 "transmembrane domain 1"
XX Domain 67..87 "transmembrane domain 2"
XX Domain 103..124 "transmembrane domain 3"
XX Domain 142..167 "transmembrane domain 4"
XX
XX WO9854317-A1.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-EP003437.
XX
XX 30-MAY-1997; 97US-0048057P.
XX
XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
XX
XX WPI; 1999-059835/05.
XX N-PSDB; AAV84159.
XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
XX resistance of CCR5-expressing cells to HIV-1 infection.
XX Disclosure; Page 38-39; 55pp; English.
XX This is the amino acid sequence of a CCR5 variant protein, designated
XX CCR5-delta32, that includes the first 4 transmembrane domains of wild-
XX type CCR5 (see AAW88232), but lacks transmembrane domains 5-7. CCR5
XX serves as a co-receptor for infection by macrophage-tropic (M-tropic)
XX strains of HIV-1. Individuals homozygous for the CCR5-delta32 mutation
XX are resistant to HIV-1 infection, but heterozygous individuals are
XX susceptible. The invention additionally relates to the identification of
XX variant CCR5s303 (see AAW88231), which lacks transmembrane domains 3-7 of
XX CCR5. The detection of CCR5 variants may be used to identify individuals
XX at lower risk of infection relative to the general population who, if
XX infected, may exhibit slower progression to AIDS. Probes and primers (see
XX AAV84127-36) are provided for use in diagnostic methods for detecting the
XX presence of such variants. A method is provided for inhibiting HIV-1
XX infection of a cell expressing the CCR5 receptor. This involves
XX introducing a nucleic acid encoding a CCR5 variant into the cell, thereby
XX reducing the number of functional CCR5 molecules present on the cell
XX surface
XX
XX Sequence 215 AA;
Query Match 100.0%; Score 126; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 5
ADC10142
ID ADC10142 standard; protein; 268 AA.
XX ADC10142;
XX
XX 18-DEC-2003 (first entry)
XX Human NOVX polypeptide SEQ ID NO: 162.
XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
XX antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
XX pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
XX inflammatory disorder; chromosome mapping; tissue typing;
XX predictive medicine.
XX Homo sapiens.
XX WO2003000842-A2.
XX
XX 03-JAN-2003.
XX
XX 04-JUN-2002; 2002WO-US017443.
XX
XX 04-JUN-2001; 2001US-0295607P.
XX 04-JUN-2001; 2001US-0295661P.
XX 06-JUN-2001; 2001US-0296404P.
XX 06-JUN-2001; 2001US-0296418P.
XX 07-JUN-2001; 2001US-0296575P.
XX 11-JUN-2001; 2001US-0297414P.
XX 12-JUN-2001; 2001US-0295573P.
XX 12-JUN-2001; 2001US-0297567P.
XX 14-JUN-2001; 2001US-0298285P.
XX 15-JUN-2001; 2001US-0298528P.
XX 18-JUN-2001; 2001US-0299133P.

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19-JUN-2001; 2001US-0299230P.
PR 21-JUN-2001; 2001US-029949P.
PR 26-JUN-2001; 2001US-0300177P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 30-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-0308890P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324669P.
PR 03-DEC-2001; 2001US-0337477P.
PR 14-DEC-2001; 2001US-0341562P.
PR 21-FEB-2002; 2002US-0358656P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 22-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359864P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-0379444.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Bainger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JM, Hjalte T, Ji W, Kekuda R;
PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
XX WPI; 2003-210149/20.
DR N-PSDB; ADC10144.
XX
XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-

AC ADC10144;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human NOVX polypeptide SEQ ID NO: 164.
XX
XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
XX antiinflammatory; gene therapy; antisense therapy; thymimetic; NOVA;
XX pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
XX inflammatory disorder; chromosome mapping; tissue typing;
XX predictive medicine.
XX
XX Homo sapiens.
XX
XX WO2003000842-A2.
XX
XX 03-JAN-2003.
XX
XX 04-JUN-2002; 2002WO-US017443.
XX
XX 04-JUN-2001; 2001US-0295607P.
XX 04-JUN-2001; 2001US-0295661P.
XX 06-JUN-2001; 2001US-0296404P.
XX 06-JUN-2001; 2001US-0296418P.
XX 07-JUN-2001; 2001US-0296575P.
XX 11-JUN-2001; 2001US-0297414P.
XX 12-JUN-2001; 2001US-0295573P.
XX 12-JUN-2001; 2001US-0297567P.
XX 14-JUN-2001; 2001US-0298285P.
XX 15-JUN-2001; 2001US-0298528P.
XX 18-JUN-2001; 2001US-0299133P.
XX 19-JUN-2001; 2001US-0299230P.
XX 21-JUN-2001; 2001US-0299949P.
XX 22-JUN-2001; 2001US-0300177P.
XX 26-JUN-2001; 2001US-0300883P.
XX 28-JUN-2001; 2001US-0301530P.
XX 28-JUN-2001; 2001US-0301550P.
XX 03-JUL-2001; 2001US-0302951P.
XX 31-JUL-2001; 2001US-0308890P.
XX 14-SEP-2001; 2001US-0322297P.
XX 25-SEP-2001; 2001US-0324669P.
XX 03-DEC-2001; 2001US-0337477P.
XX 14-DEC-2001; 2001US-0341562P.
XX 21-FEB-2002; 2002US-0358656P.
XX 21-FEB-2002; 2002US-0359122P.
XX 22-FEB-2002; 2002US-0358978P.
XX 22-FEB-2002; 2002US-0359034P.
XX 22-FEB-2002; 2002US-0359035P.
XX 22-FEB-2002; 2002US-0359121P.
XX 27-FEB-2002; 2002US-0359864P.
XX 01-MAR-2002; 2002US-0360858P.
XX 12-MAR-2002; 2002US-0363430P.
XX 10-APR-2002; 2002US-0371346P.
XX 10-MAY-2002; 2002US-0379444P.
XX 04-JUN-2002; 2002US-0379444.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Bainger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JM, Hjalte T, Ji W, Kekuda R;
PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
XX WPI; 2003-210149/20.
DR N-PSDB; ADC10144.
XX
XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-

Query Match 100.0%; Score 126; DB 7; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTWCQLTGLYPIGFFS 22
DB 93 QWDFGNTWCQLTGLYPIGFFS 114
RESULT 6
ADC10144
ID ADC10144 standard; protein; 268 AA.
XX

PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 XX or CNS diseases.

PS Claim 1; SEQ ID NO 164; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.

XX Sequence 268 AA;

Query Match 100.0%; Score 126; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 |||||
 Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 7

AAW26766
 ID AAW26766 standard; protein; 332 AA.

XX AAW26766;

XX 21-MAY-1998 (first entry)

XX Human chemokine receptor MMLR-CCR.

XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;
 KW monocyte; macrophage; chemotaxis; haematopoiesis; infection;
 KW inflammation; proliferative disease; cardiovascular disease; tumour;
 KW rheumatoid arthritis; alveolitis; atherosclerosis;
 KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;
 KW inflammatory bowel disease; toxic shock syndrome; septic shock;
 KW Chediak-Higashi syndrome; therapy; diagnosis.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 107..128

XX Peptide /note= "conserved peptide"

XX Misc-difference 121
 XX /note= "a claimed polypeptide has isoleucine at residue
 121"

XX WO9741225-A2.

XX 06-NOV-1997.

XX 25-APR-1997; 97WO-US006993.

XX 26-APR-1996; 96US-00638081.

XX (INCY) INCYTE PHARM INC.

XX Au-Young J, Bandman O, Coleman R, Wilde CG;

XX WPI; 1997-549729/50.

XX N-PSDB; AAT99542.

XX Polynucleotide encoding MMLR-CCR or MPH-CCR chemokine receptor - useful
 PT to study, diagnose and treat, e.g. infection, inflammation, solid tumour
 PT and proliferative and cardiovascular disease.

PS Claim 8; Page 37-38; 59pp; English.

XX This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
 CC associated with monocyte/macrophage infiltration and chemotaxis and
 CC haematopoiesis. The amino acid sequence was deduced from a cDNA clone
 CC (see AAT99542) obtained from a cDNA library made from mononuclear cells
 CC collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
 CC with inflammation and immunomodulation. Another novel chemokine receptor,
 CC MPH-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7
 CC transmembrane spanning segments connected by a series of intracellular
 CC and extracellular loops. MMLR-CCR and MPH-CCR can be used to study, is
 CC diagnose and treat disease states or inappropriate activation via
 CC perturbed by normal leukopoiesis or infection, inflammation,
 CC chemokine agonists or antagonists, such as infection, inflammation,
 CC proliferative disease, tumorigenesis, autoimmune disease, rheumatoid
 CC arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
 CC asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
 CC shock syndrome, septic shock and Chediak-Higashi syndrome

XX Sequence 332 AA;

Query Match 100.0%; Score 126; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 |||||
 Db 84 QWDFGNTMCQLLTGLYFIFGFFS 105

RESULT 8

AAW27407

ID AAW27407 standard; protein; 352 AA.

XX AAW27407;

XX 14-APR-1998 (first entry)

XX Human CCR5.

XX Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX WO9732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-BE000023.

XX 01-MAR-1996; 96EP-00870021.

XX 06-AUG-1996; 96EP-00870102.

XX (EURO-) EUROSREEN SA.

XX Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

XX N-PSDB; AAT90117.

XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.

XX Claim 4; Fig 1b-c; 94pp; English.

XX The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but

CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 |||||
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
 RESULT 9
 AAW27123
 ID AAW27123 standard; protein; 352 AA.
 XX AC AAW27123;
 XX DT 14-DEC-1997 (first entry)
 XX DE Human chemokine receptor 88C.
 XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 XX KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
 XX KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 XX KW modulator; antibody; human.
 XX OS Homo sapiens.
 XX PH Key
 FT Domain 1..32 Location/Qualifiers
 FT /label= Extracellular_domain
 FT Domain 56..67
 FT /label= Intracellular_domain
 FT Domain 89..112
 FT /label= Extracellular_domain
 FT Domain 125..145
 FT /label= Intracellular_domain
 FT Domain 166..191
 FT /label= Extracellular_domain
 FT Domain 213..235
 FT /label= Intracellular_domain
 FT Domain 259..280
 FT /label= Extracellular_domain
 FT Domain 301..352
 FT /label= Intracellular_domain
 XX PN WO9722698-A2.
 XX PD 26-JUN-1997.
 XX PF 20-DEC-1996; 96WO-US020759.
 XX PR 20-DEC-1995; 95US-00575967.
 XX PR 07-JUN-1996; 96US-00661393.
 XX XX (ICOS-) ICOS CORP.
 XX Gray PW, Schweickart VL, Raport CU;
 XX WPI; 1997-341689/31.
 XX DR N-PSDB; AAT85161.
 XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 XX modulate leukocyte trafficking, e.g. for treatment of inflammation,

PT tumours, viral infections, auto-immune diseases, etc.
 XX Claim 16; Page 47-48; 65pp; English.
 XX This polypeptide sequence comprises novel human chemokine receptor 88C, a
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
 CC macrophage library. It shows 62% identity to CCR1. Chemokine receptor
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
 CC and their polypeptide fragments can be produced in transformed host
 CC cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 |||||
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
 RESULT 10
 AAW27125
 ID AAW27125 standard; protein; 352 AA.
 XX AC AAW27125;
 XX DT 14-DEC-1997 (first entry)
 XX DE Macaque chemokine receptor 88C.
 XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 XX KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
 XX KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 XX KW modulator; antibody.
 XX OS Macaca sp.
 XX PN WO9722698-A2.
 XX PD 26-JUN-1997.
 XX PF 20-DEC-1996; 96WO-US020759.
 XX PR 20-DEC-1995; 95US-00575967.
 XX PR 07-JUN-1996; 96US-00661393.
 XX XX (ICOS-) ICOS CORP.
 XX Gray PW, Schweickart VL, Raport CU;
 XX WPI; 1997-341689/31.
 XX DR N-PSDB; AAT85163.
 XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
 XX tumours, viral infections, auto-immune diseases, etc.
 XX Claim 36; Page 57-58; 65pp; English.
 XX This polypeptide sequence comprises macaque chemokine receptor 88C, a G
 CC protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
 CC amplification. It shows 97% identity to human 88C (AAW27123). 88C
 CC receptors and their polypeptide fragments can be produced in transformed

CC host cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc. A hybridoma that produces an
 CC antibody that specifically binds to macaque 88C is claimed
 XX
 XX SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22
 DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

RESULT 11
 AAW07602
 ID AAW07602 standard; protein; 352 AA.

AC AAW07602;
 XX 26-FEB-1997 (first entry)
 DT Human G-protein chemokine receptor HDGNR10.

XX G-protein chemokine receptor; HDGNR10; signal transduction;
 KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
 KW therapy.

OS Homo sapiens.

XX WO9639437-A1.

PN 12-DEC-1996.

XX 06-JUN-1995; 95WO-US007173.

XX 06-JUN-1995; 95WO-US007173.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI; 1997-043072/04.

XX N-PSDB; AAT44042.

XX Human G-protein chemokine receptor, HDGNR10 - useful to identify
 PT (antagonists, for treatment of haematopoiesis, leukaemia, chronic and
 PT acute inflammation, rheumatoid arthritis, etc.

XX Claim 1; Page 44-46; 61pp; English.

XX Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7
 CC -transmembrane protein involved in signal transduction. Its amino acid
 CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human
 CC monocyte library. Isolation of the cDNA allows prodn. of recombinant
 CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
 CC receptor can be used to identify agonists or antagonists of the receptor;
 CC such cpds. can be used to treat conditions related to the under- and over
 CC -expression of G-protein chemokine receptors
 XX

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22

DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

RESULT 12

AAW23835

ID AAW23835 standard; protein; 352 AA.

XX AAW23835;

XX 08-JUN-1998 (first entry)

DE Human CC chemokine receptor 5 (CCR5).

KW CQ chemokine receptor 5; CCR5; G-protein coupled receptor;
 KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.

OS Homo sapiens.

XX Location/Qualifiers

XX 29..55

XX /label= I

XX /note= "transmembrane domain"

XX 104..126

XX /label= III

XX /note= "transmembrane domain"

XX 109..120

XX /note= "extracellular loop-1 (Claim 19)"

XX 143..171

XX /label= IV

XX /note= "transmembrane domain"

XX 187..210

XX /note= "extracellular loop-2 (Claim 19)"

XX 194..219

XX /label= V

XX /note= "transmembrane domain"

XX 238..258

XX /label= VI

XX /note= "transmembrane domain"

XX 261..276

XX /note= "extracellular loop-3 (Claim 19)"

XX 277..300

XX /label= VII

XX /note= "transmembrane domain"

XX WO9745543-A2.

XX 04-DEC-1997.

XX 28-MAY-1997; 97WO-US009586.

XX 28-MAY-1996; 96US-0018508P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;

XX Broder CC, Kennedy PE;

XX WPI; 1998-032650/03.

XX N-PSDB; AAT76920.

XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 XX between HIV and a target cell.

XX Claim 68; Fig 1C; 70pp; English.

XX This protein sequence comprises of a novel human macrophage-selective CC
 CC chemokine receptor that has been designated CCR5. The sequence was
 CC deduced from an isolated cDNA clone (see AAT76920). An Alu27Leu variant
 CC (see W238340 of CCR5 was also identified. The susceptibility of human
 CC macrophages to HIV infection depends on cell surface expression of CD4
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
 CC protein coupled cell surface molecules. It plays an essential role in the

CC membrane fusion step of infection by some HIV isolates. The establishment
 CC of stable, non-human cell lines and transgenic mammals having cells that
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 CC agents capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 13
 AAW88232
 ID AAW88232 standard; protein; 352 AA.

XX AC AAW88232;

XX DT 15-MAR-1999 (first entry)

XX DE HIV-1 co-receptor CCR5.

XX KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Domain 32...56

FT /note= "transmembrane domain 1"

FT Domain 67...87

FT /note= "transmembrane domain 2"

FT Misc-difference 101

FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 (stop) in CCR5m303"

FT Domain 103...124

FT /note= "transmembrane domain 3"

FT Domain 142...167

FT /note= "transmembrane domain 4"

FT Domain 200...223

FT /note= "transmembrane domain 5"

FT Domain 236...260

FT /note= "transmembrane domain 6"

FT Domain 275...301

FT /note= "transmembrane domain 7"

XX WO9854317-A1.

XX XX 03-DEC-1998.

XX XX 29-MAY-1998; 98WO-BP003437.

XX XX 30-MAY-1997; 97US-0048057P.

XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX Beretta A, Quillent C, Arenzana Slesados F, Braun J;

XX WPI; 1999-059835/05.

XX N-PSDB; AAV84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 XX resistance of CCR5-expressing cells to HIV-1 infection.

XX Disclosure; Page 34-35; 55pp; English.

XX

CC This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAW88231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 14

AAW80128

ID AAY80128 standard; protein; 352 AA.

XX AC AAY80128;

XX DT 19-MAY-2000 (first entry)

XX Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.

XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumour; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.

XX OS Homo sapiens.

XX US6025154-A.

XX 15-FEB-2000.

XX 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI; 2000-181807/16.

XX N-PSDB; AAZ91481.

XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 XX for diagnostic assays, scientific research and screening for compounds
 XX which bind to and activate or inhibit activation of the receptor
 XX polypeptides.

XX Claim 1; Fig 1; 22pp; English.

XX The present sequence represents a human G-protein chemokine receptor
 CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 CC screening for compounds which bind to and either: (1) activate the
 CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound

CC healing, coagulation, and angiogenesis; treatment of solid tumours,
 CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 CC parasitic infections, psoriasis, and to stimulate growth factor activity;
 CC or (2) inhibit activation of the HDGFR10 polypeptides which is useful for
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
 CC diagnostic assays for detecting diseases related to mutations in the
 CC nucleic acid sequences encoding the polypeptides and for detecting an
 CC altered level of the soluble form of the receptor polypeptides. The
 CC polynucleotides are also useful for in vitro purposes related to
 CC scientific research, synthesis of DNA and manufacture of DNA vectors
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 126; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 15
 AAG79089
 ID AAG79089 standard; protein; 352 AA.
 XX
 AC AAG79089;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Amino acid sequence of human CCR5 protein.
 XX
 KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX
 OS Homo sapiens.
 XX
 PN WO200164752-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006322.
 XX
 PR 02-MAR-2000; 2000US-00517605.
 XX
 PA (UJNY) UNIV NEW YORK STATE.
 PA (UJNY-) UNIV NIJMEGEN.
 XX
 PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX
 DR WPI; 2001-602565/68.
 XX
 PT An antibody for the treatment or prevention of HIV-infection comprises a
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 PT DC-SIGN due to concomitant conformational change.
 XX
 PS Disclosure; Page 118-119; 131pp; English.
 XX
 CC The specification describes an antibody which is specific for an
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human CCR5 protein, which is

CC a translocation promoting agent that interacts with CD4. This receptor
 CC functions in HIV-1 entry into cells
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 16
 AAE07046
 ID AAE07046 standard; protein; 352 AA.
 XX
 AC AAE07046;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGFR10 protein #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGFR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neutropenic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 Domain 1..36
 /label= Extracellular_domain
 Domain 37..305
 /label= Transmembrane_domain
 Domain 37..58
 /label= Transmembrane_domain
 /note= "Segment 1"
 Domain 59..67
 /label= Intracellular_loop_1
 Domain 68..88
 /label= Transmembrane_domain
 /note= "Segment 2"
 Domain 89..102
 /label= Extracellular_loop_1
 Domain 103..124
 /label= Transmembrane_domain
 /note= "Segment 3"
 Domain 125..141
 /label= Intracellular_loop_2
 Domain 142..166
 /label= Transmembrane_domain
 /note= "Segment 4"
 Domain 167..195
 /label= Extracellular_loop_2
 Domain 196..223
 /label= Transmembrane_domain
 /note= "Segment 5"
 Domain 224..235
 /label= Intracellular_loop_3
 Domain 236..260
 /label= Transmembrane_domain
 /note= "Segment 6"
 Domain 261..274
 /label= Extracellular_loop_3
 Domain 287..305
 /label= Transmembrane_domain
 FT

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FT      /note= "Segment 7"
FT      306, 352
FT      /label= Intracellular_domain
XX
PN      WO200158916-A2.
PD      16-AUG-2001.
XX
XX      09-FEB-2001; 2001WO-US004153.
XX
XX      09-FEB-2000; 2000US-0181258P.
XX      09-MAR-2000; 2000US-0187999P.
XX      22-SEP-2000; 2000US-0234336P.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
XX
XX      Rosen CA, Roschke V, Li Y, Ruben SM;
XX      WPI; 2001-488966/53.
XX      N-PSDB; AAD13282.
XX
XX      Isolated nucleic acid encoding a human G-protein chemokine receptor
XX      (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
XX      diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
XX      neurodegenerative disorders.
XX
XX      Claim 102; Fig 1; 518pp; English.
XX
XX      The invention relates to human G-protein chemokine receptor (CCR5)
XX      HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
XX      useful for treating, preventing or ameliorating a disease or disorder
XX      associated with inflammation, defective or aberrant chemotaxis of immune
XX      cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
XX      sarcoma) or defective or aberrant T-cell antigen presenting cell
XX      interaction. The disease or disorder may also be an infectious disease
XX      (e.g. a viral infection such as an early stage HIV infection, a
XX      cytomegalovirus infection, or a poxvirus infection), an autoimmune
XX      disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
XX      disease or disorder may be associated with aberrant CCR5 expression, lack
XX      of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
XX      function. CCR5 HDGNR10 protein is used as a food additive or preservative
XX      to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
XX      for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
XX      protein, antibodies, agonists and antagonists are also useful in the
XX      diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
XX      gland, bone, bone marrow, gastrointestinal tract, liver, lung,
XX      urogenital); immune disorders (Addison's disease, allergies, autoimmune
XX      haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX      disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
XX      ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
XX      present sequence is human CCR5 HDGNR10 protein
XX
XX      Sequence 352 AA;
XX
XX      Query Match      100.0%; Score 126; DB 4; Length 352;
XX      Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX      Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 QWDFGNTMCQLLTGLYFTGFPS 22
XX      DB      93 QWDFGNTMCQLLTGLYFTGFPS 114
XX
XX      RESULT 17
XX      AAE07048
XX      ID      AAE07048 standard; protein; 352 AA.
XX      AC
XX      XX      AAE07048;
XX      DT      16-OCT-2001 (first entry)
XX      DE      Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX

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KW      Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW      human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
KW      cystostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
KW      neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW      rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW      gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW      haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW      multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW      cardiovascular disorder; myocardial ischaemia.
XX
XX      Homo sapiens.
XX
XX      WO200158916-A2.
XX      16-AUG-2001.
XX
XX      09-FEB-2001; 2001WO-US004153.
XX
XX      09-FEB-2000; 2000US-0181258P.
XX      09-MAR-2000; 2000US-0187999P.
XX      22-SEP-2000; 2000US-0234336P.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
XX
XX      Rosen CA, Roschke V, Li Y, Ruben SM;
XX      WPI; 2001-488966/53.
XX      N-PSDB; AAD13299.
XX
XX      Isolated nucleic acid encoding a human G-protein chemokine receptor
XX      (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
XX      diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
XX      neurodegenerative disorders.
XX
XX      Example 40; Page 504-505; 518pp; English.
XX
XX      The invention relates to human G-protein chemokine receptor (CCR5)
XX      HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
XX      useful for treating, preventing or ameliorating a disease or disorder
XX      associated with inflammation, defective or aberrant chemotaxis of immune
XX      cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
XX      sarcoma) or defective or aberrant T-cell antigen presenting cell
XX      interaction. The disease or disorder may also be an infectious disease
XX      (e.g. a viral infection such as an early stage HIV infection, a
XX      cytomegalovirus infection, or a poxvirus infection), an autoimmune
XX      disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
XX      disease or disorder may be associated with aberrant CCR5 expression, lack
XX      of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
XX      function. CCR5 HDGNR10 protein is used as a food additive or preservative
XX      to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
XX      for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
XX      protein, antibodies, agonists and antagonists are also useful in the
XX      diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
XX      gland, bone, bone marrow, gastrointestinal tract, liver, lung,
XX      urogenital); immune disorders (Addison's disease, allergies, autoimmune
XX      haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
XX      disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
XX      ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
XX      present sequence is human CCR5 HDGNR10 protein
XX
XX      Sequence 352 AA;
XX
XX      Query Match      100.0%; Score 126; DB 4; Length 352;
XX      Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX      Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 QWDFGNTMCQLLTGLYFTGFPS 22
XX      DB      93 QWDFGNTMCQLLTGLYFTGFPS 114
XX
XX      RESULT 18
XX      AAG80111

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ID AAG80111 standard; protein; 352 AA.
 AC AAG80111;
 XX
 DT 17-JAN-2002 (first entry)
 XX
 DE Human CCR5 protein.
 XX
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 XX inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cystostatic;
 KW antiinflammatory; antiaschmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 PN W0200172830-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 02-APR-2001; 2001WO-EP003708.
 XX
 PR 31-MAR-2000; 2000DE-01016013.
 XX
 PA (JFPP-) IPF PHARM GMBH.
 PA (FORS/) FORSMANN U.
 XX
 PI Forssmann W, Adermann K, Heitland A, Spodsborg N;
 XX
 DR WPI; 2001-626256/72.
 XX
 PT Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX
 PS Disclosure; Page 10; 26pp; German.
 XX
 CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cystostatic, antiinflammatory, antiaschmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLGLYFIFGFFS 22
 DB 93 QWDFGNTWCQLLGLYFIFGFFS 114
 RESULT 19
 AAE04321
 ID AAE04321 standard; protein; 352 AA.
 XX
 AC AAE04321;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cystostatic; immunosuppressive; neoprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 XX

DE Human chemokine receptor (CCR), CC-CCR-5 related protein #2.
 XX
 KW Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CCR-5; envelope glycoprotein; anti-HIV.
 XX
 OS Homo sapiens.
 XX
 PN US6258527-B1.
 XX
 PD 10-JUL-2001.
 XX
 PF 21-MAY-1997; 97US-00861105.
 XX
 PR 20-MAY-1996; 96US-0017157P.
 PR 19-JUN-1996; 96US-0020043P.
 PR 19-MAY-1997; 97US-00858660.
 XX
 PA (AARO-) AARON DIAMOND AIDS RES CENT.
 PA (UTNY) UNIV NEW YORK STATE.
 XX
 PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;
 XX
 DR WPI; 2001-417127/44.
 DR N-PSDB; AAD08577.
 XX
 PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of
 PT HIV.
 XX
 PS Disclosure; Col 47-50; 37pp; English.
 XX
 CC The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR). CC-CCR-5 related protein.
 CC CC-CCR-5 is the principal cofactor for entry mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCQLLGLYFIFGFFS 22
 DB 93 QWDFGNTWCQLLGLYFIFGFFS 114
 RESULT 20
 AAE07037
 ID AAE07037 standard; protein; 352 AA.
 XX
 AC AAE07037;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cystostatic; immunosuppressive; neoprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 XX

XX rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Domain 1..36
 FT Domain /label= Extracellular_domain
 FT Domain 37..305
 FT Domain /label= Transmembrane_domain
 FT Domain 37..58
 FT Domain /label= Transmembrane_domain
 FT Domain /note= "Segment 1"
 FT Domain 59..67
 FT Domain /label= Intracellular_loop_1
 FT Domain 68..88
 FT Domain /label= Transmembrane_domain
 FT Domain /note= "Segment 2"
 FT Domain 89..102
 FT Domain /label= Extracellular_loop_1
 FT Domain 103..124
 FT Domain /label= Transmembrane_domain
 FT Domain /note= "Segment 3"
 FT Domain 125..141
 FT Domain /label= Intracellular_loop_2
 FT Domain 142..166
 FT Domain /label= Transmembrane_domain
 FT Domain /note= "Segment 4"
 FT Domain 167..195
 FT Domain /label= Extracellular_loop_2
 FT Domain 196..223
 FT Domain /label= Transmembrane_domain
 FT Domain /note= "Segment 5"
 FT Domain 224..235
 FT Domain /label= Intracellular_loop_3
 FT Domain 236..260
 FT Domain /label= Transmembrane_domain
 FT Domain /note= "Segment 6"
 FT Domain 261..274
 FT Domain /label= Extracellular_loop_3
 FT Domain 287..305
 FT Domain /label= Transmembrane_domain
 FT Domain /note= "Segment 7"
 FT Domain 306..352
 FT Domain /label= Intracellular_domain

XX WO200158915-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488965/53.

XX N-PSDB; AADI3181.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 neurodegenerative disorders.

XX Claim 102; Fig 1; 495pp; English.

CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemia) and wound
 CC healing
 XX

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLLTGLYTFGFFS 22
 |||||
 Db 93 QWDFGNTMQLLTGLYTFGFFS 114

RESULT 21

AAE07039

ID AAE07039 standard; protein; 352 AA.

XX AC AAE07039;

XX DT 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 XX human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 XX cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 XX neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 XX rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 XX gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 XX haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 XX multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 XX cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158915-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488965/53.

XX N-PSDB; AADI3196.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
PT neurodegenerative disorders.
XX
XX Example 40; Page 486-487; 495pp; English.
XX
XX The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10
CC protein. CCR5 HDGMR10 antibodies are useful for treating, preventing or
CC ameliorating a disease or disorder associated with inflammation, such as
CC defective or aberrant chemotaxis of immune cells, HIV infection, such as
CC Pneumocystis carinii pneumonia or Kaposi's sarcoma, HIV infection, such as
CC aberrant T-cell antigen presenting cell interaction. The disease or
CC disorder may also be an infectious disease (e.g. a viral infection such
CC as an early stage HIV infection, a cytomegalovirus infection, or a
CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
CC a neurodegenerative disorder. The disease or disorder may be associated
CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGMR10 protein
CC is used as a food additive or preservative to increase or decrease
CC storage capabilities. CCR5 HDGMR10 DNA are useful for chromosome
CC identification and in gene therapy. CCR5 HDGMR10 DNA, protein,
CC antibodies, agonists and antagonists are also useful in the diagnosis,
CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
CC autoimmune rheumatoid arthritis, diabetes mellitus, Crohn's disease, multiple
CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
CC disorders (myocardial ischaemias) and wound healing
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 126; DB 4; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
XX DB 93 QWDFGNTWCQLLTGLYFIFGFFS 114
XX
XX RESULT 22
XX AAB46858
XX ID AAB46858 standard; protein; 352 AA.
XX AC AAB46858;
XX
XX 16-AUG-2001 (revised)
XX DT 02-AUG-2001 (revised)
XX DT 04-MAY-2001 (first entry)
XX
XX DE Human HDGMR10 protein.
XX
XX HDGMR10; human; G-protein chemokine receptor; antiinflammatory;
XX immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
XX cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
XX vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
XX angiogenesis; solid tumour; infection; leukemia; growth factor activity;
XX T-cell mediated autoimmune disease; psoriasis; allergy; atherosclerosis;
XX anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
XX immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
XX prostaglandin-independent fever; bone marrow failure; sarcoidosis;
XX hyper-eosinophilic syndrome; vulnary.
XX
XX Homo sapiens.
XX OS
XX
XX US2001000241-A1.
XX PN
XX
XX 12-APR-2001.
XX PD
XX
XX 29-NOV-2000; 2000US-00725285.
XX PF
XX
XX

PR 06-JUN-1995; 95US-00466343.
PR 18-NOV-1998; 98US-00195662.
PR 25-JUN-1999; 99US-00339912.
XX (LIYY/) LI Y.
PA (RUBB/) RUBEN S M.
XX
XX Li Y, Ruben SM;
XX
XX WPI: 2001-226317/23.
XX N-PSDB; AAF26390.
XX
XX New human G-protein chemokine receptor polypeptides and polynucleotides,
XX useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX
XX Claim 1a; Page 15; 22pp; English.
XX
XX This invention describes a novel receptor polypeptide (I) selected from
XX (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
XX specification; and (ii) a polypeptide encoded by the cDNA contained in a
XX plasmid, and fragments, analogs and derivatives of the polypeptide. The
XX products of the invention have antiinflammatory, immunomodulatory,
XX anticoagulant, antiallergic, immunosuppressive, vulnary, cytostatic,
XX antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
XX activity and can be used for gene therapy. The G-protein chemokine
XX receptors, HDGMR10, (I) are useful for screening for compounds which
XX activate or inhibit activation of (I). The products of the invention can
XX also be used for stimulating haematopoiesis, wound healing, coagulation,
XX angiogenesis, treating solid tumours, chronic infections, leukemia, T-
XX cell mediated autoimmune diseases, parasitic infections, psoriasis, and
XX stimulating growth factor activity. HDGMR10 is useful for treating
XX allergy, atherosclerosis, anaphylaxis, malignancy, chronic and acute
XX inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
XX reactions, prostaglandin-independent fever, bone marrow failure,
XX silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
XX eosinophilic syndrome. (N.B. This record was resubmitted to correct
XX errors in the keyword formatting)
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 126; DB 4; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
XX DB 93 QWDFGNTWCQLLTGLYFIFGFFS 114
XX
XX RESULT 23
XX ABB56342
XX ID ABB56342 standard; protein; 352 AA.
XX XX
XX AC ABB56342;
XX
XX 18-FEB-2002 (first entry)
XX DT
XX
XX Non-endogenous human GPCR protein, SEQ ID NO: 477.
XX
XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
XX constitutively activated GPCR; agonist; disease.
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX WO20017172-A2.
XX PN
XX
XX 18-OCT-2001.
XX PD
XX
XX 05-APR-2001; 2001WO-US011098.
XX PF
XX
XX 07-APR-2000; 2000US-0195747P.
XX PR
XX

PA (AREN-) ARENA PHARM INC.
 XX Lehmann-Bruinsma K, Liaw CW, Lin I;
 XX WPI; 2001-648759/74.
 DR N-PSDB; ARI97978.
 XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 of GPCRs.
 XX Claim 1; Page 277-278; 394pp; English.
 XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR
 XX
 XX Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
 RESULT 24
 AAB83354
 ID AAB83354 standard; protein; 352 AA.
 AC AAB83354;
 XX 09-OCT-2001 (first entry)
 DT Human CCR5 protein sequence.
 DE Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 KW human immunodeficiency virus; anti-inflammatory disease; human.
 XX Homo sapiens.
 OS EP1118858-A2.
 PN 25-JUL-2001.
 PD 03-JAN-2001; 2001EP-00300020.
 XX 12-JAN-2000; 2000GB-00000659.
 PR 12-JAN-2000; 2000GB-00000661.
 PR 12-JAN-2000; 2000GB-00000663.
 XX (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX Dobbs S, Perros M, Rickett GA;
 XX WPI; 2001-477088/52.
 DR N-PSDB; AAF87099.
 XX Determining if an agent can modulate CCR5-gp120 interaction, comprises
 PT incubating the agent with CCR5 and gp120 and determining if the agent
 PT modulates the interaction.
 XX Claim 1; Page 110; 113pp; English.
 PS This sequence represents the human CCR5 protein sequence. The invention
 CC relates to a method for determining whether an agent is capable of

CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5.
 XX Sequence 352 AA;
 Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114
 RESULT 25
 AAB82948
 ID AAB82948 standard; protein; 352 AA.
 AC AAB82948;
 XX 21-DEC-2001 (first entry)
 DT Human HIV-1 co-receptor CCR5.
 DE CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 KW infection; therapy; vaccine; anti-HIV-1.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 FH Binding-site 2..18 /note= "binds to HIV-1 gp120"
 FT WO200164710-A2.
 XX 07-SEP-2001.
 PD 28-FEB-2001; 2001WO-US006699.
 XX 29-FEB-2000; 2000US-0185667P.
 PR 19-MAY-2000; 2000US-0205839P.
 PR 07-FEB-2001; 2001US-0267231P.
 XX (PROG-) PROGENICS PHARM INC.
 PA (AARO-) AARON DIAMOND AIDS RES CENT.
 XX Dragic T, Olson WC;
 XX WPI; 2001-611273/70.
 DR N-PSDB; AAR26903.
 XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
 PT receptor) amino terminal domain including negatively charged and two
 PT sulfated tyrosine residues is useful for treating HIV infection in
 PT humans.
 XX Claim 1; Page 30; 163pp; English.
 PS The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
 CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
 CC site that determines the specificity of the interaction between CCR5 and
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the

CC CCR5 N-terminus is required for gp120 binding and may critically modulate
 CC the susceptibility of target cells to HIV-1 infection in vivo. The
 CC invention provides claimed sulfated peptides (see A882947) that are
 CC based on the CCR5 N-terminal region and which are effective for
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
 CC cells from becoming infected with HIV, of treating a subject whose CD4+
 CC cells are infected with HIV, and of identifying an agent which inhibits
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
 CC out in a subject, especially a human, infected (therapeutic method), not
 CC infected with HIV (prophylactic method), or in a subject who is not
 CC infected with, but has been exposed to, HIV
 XX
 XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
 |||||
 Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 26

AAU97150
 ID AAU97150 standard; protein; 352 AA.

AC AAU97150;

DT 13-AUG-2002 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.

XX Homo sapiens.

OS US2002048786-A1.

PN 25-APR-2002.

PD 09-FEB-2001; 2001US-00779879.

PF 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.

PA (ROSC/) ROSCHKE V.

PA (LIY/) LI Y.

PA (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

PI WPI; 2002-434754/46.

XX N-PSDB; ABK51853.

DR New nucleic acid encoding an antibody specific for the G-protein
 XX chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 XX inflammation.

PT Claim 61; Fig 1; 180pp; English.

XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune

CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #1
 XX
 XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
 |||||
 Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 27

AAU97152

ID AAU97152 standard; protein; 352 AA.

XX AC AAU97152;

XX DT 13-AUG-2002 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.

XX Homo sapiens.

OS US2002048786-A1.

PN 25-APR-2002.

PD 09-FEB-2001; 2001US-00779879.

PF 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.

PA (ROSC/) ROSCHKE V.

PA (LIY/) LI Y.

PA (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

PI WPI; 2002-434754/46.

XX N-PSDB; ABK51870.

DR New nucleic acid encoding an antibody specific for the G-protein
 XX chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 XX inflammation.

PT Disclosure; Page 165-166; 180pp; English.

XX The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide

CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #2
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
 Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 28
 AAM52829
 ID AAM52829 standard; protein; 352 AA.
 XX
 AC AAM52829;

DT 22-FEB-2002 (first entry)
 DE Human CCR5 Gln 55 variant.

KW CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification; variant.

OS Homo sapiens.

XX Key Location/Qualifiers

FF Misc-difference 55

FT FT /note= "Glu replaces wild-type Leu; encoded by CTG"

FT Misc-difference 58

FT FT /note= "Encoded by AGC"

XX WO200171346-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009155.

XX 21-MAR-2000; 2000US-0190946P.

PR 21-MAR-2000; 2000US-0190996P.

PR 21-MAR-2000; 2000US-0191299P.

PR 20-MAR-2001; 2001US-00813448.

PR 20-MAR-2001; 2001US-00813651.

PR 20-MAR-2001; 2001US-00813653.

XX (CONS-) CONSENSUS PHARM INC.

XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX WPI; 2002-010610/01.

DR N-PSDB; ABA02318.

XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 PT comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.

XX Example 3; Fig 4B; 50pp; English.

PS CC The invention relates to a method for identifying a binding compound for
 CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention,
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided method for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents a naturally occurring variant of human CCR5 in which
 CC there is a glutamine, rather than a leucine, at position 55
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
 Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 29
 AAM52828
 ID AAM52828 standard; protein; 352 AA.

XX AAM52828;

DT 22-FEB-2002 (first entry)

DE Human CC chemokine receptor 5 (CCR5).

KW CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification.

OS Homo sapiens.

XX WO200171346-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009155.

XX 21-MAR-2000; 2000US-0190946P.

PR 21-MAR-2000; 2000US-0190996P.

PR 20-MAR-2001; 2001US-00813448.

PR 20-MAR-2001; 2001US-00813651.

PR 20-MAR-2001; 2001US-00813653.

XX (CONS-) CONSENSUS PHARM INC.

XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX WPI; 2002-010610/01.

DR N-PSDB; ABA02317.

XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 PT comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.

XX Example 3; Fig 4A; 50pp; English.

XX The invention relates to a method for identifying a binding compound for
 CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention, a
 CC method for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided method for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents human CCR5
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
 |||||
 DB 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 30

ABG70597
 ID ABG70597 standard; protein; 352 AA.

AC ABG70597;

DT 03-DEC-2002 (first entry)

DE Human G-protein chemokine receptor, HDGNR10.

XX Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
 KW hematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
 KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
 KW parasitic infection; psoriasis; growth factor activity; allergy;
 KW atherosclerosis; anaphylaxis; malignancy; inflammation; histamine;
 KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
 KW prostaglandin-independent fever; bone marrow failure; shock;
 KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
 KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
 KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
 KW antipyretic; receptor.

XX Homo sapiens.

XX US2002099176-A1.

XX 25-JUL-2002.

XX 25-JUN-1999; 99US-00339912.

XX 06-JUN-1995; 95US-00466343.

XX (LIYY/) LI Y.
 PA (RUBE/) RUBEN S M.

XX Li Y, Ruben SM;

XX WPI; 2002-690494/74.

XX N-PSDB; ABS54272.

XX Novel human G-protein chemokine receptor polypeptide useful for
 PT identifying modulators for stimulating hematopoiesis, wound healing,
 PT leukemia, for treating allergy, rheumatoid arthritis, shock and as
 PT research agents.

XX Claim 7; Fig 1; 22pp; English.
 PS
 XX The present invention relates to the isolation of human G-protein
 CC chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide
 CC sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences
 CC are useful for diagnosing a disease or a susceptibility to a disease
 CC related to underexpression of HDGNR10. They are useful for identifying
 CC modulators for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or
 CC for stimulating growth factor activity. The sequences are also useful for
 CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,
 CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be
 CC used in gene therapy to treat conditions related to underexpression of
 CC HDGNR10. The present sequence represents human G-protein chemokine
 CC receptor, HDGNR10
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
 |||||
 DB 93 QWDFGNTWCQLLTGLYFIFGFFS 114

Search completed: March 4, 2004, 17:59:21
 Job time : 53.3061 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 11.2245 Seconds
(without alignments)
188.535 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFNTMCLLTGLYFIGRFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	126	100.0	352	2 A43113	chemokine (C-C) re
2	87	69.0	360	2 JC2443	chemokine (C-C) re
3	87	69.0	374	2 I38450	chemokine (C-C) re
4	82	65.1	355	2 JC5067	G protein-coupled
5	76	60.3	355	2 I43339	macrophage inflamm
6	74	58.7	356	2 I43340	MIP-1 alpha recept
7	71	56.3	355	2 I43341	chemokine (C-C) re
8	70	55.6	359	2 I43341	MIP-1 alpha recept
9	67	53.2	355	2 G02436	chemokine (C-C) re
10	66	52.4	360	2 A57160	chemokine (C-C) re
11	65	51.6	344	2 JC5942	chemokine receptor
12	65	51.6	360	2 JC4587	chemokine (C-C) re
13	60	47.6	354	2 I58186	probable G protein
14	59	46.8	369	2 JC5068	G protein-coupled
15	56	44.4	355	2 JC4304	orphan G protein-c
16	55	43.7	383	2 S55594	G protein-coupled
17	53.5	42.5	328	2 I38973	G protein-coupled
18	53	42.1	378	2 A55735	G protein-coupled
19	53	42.1	422	2 JC7080	melanin-concentrat
20	52	41.3	378	2 A45680	G protein-coupled
21	52	41.3	378	2 B55735	lymphocyte-specifi
22	51	40.5	352	1 S27357	complement C5a ana
23	50	39.7	350	2 JN0621	G protein-coupled
24	50	39.7	359	2 A48921	interleukin-8 rece
25	50	39.7	435	2 T73224	probable JNK-activ
26	50	39.7	448	2 T16256	hypothetical prote
27	49.5	39.3	359	2 I51372	angiotensin II rec
28	49	38.9	354	2 B55733	G protein-coupled
29	49	38.9	367	2 JE0349	interferon-inducib

mu opioid receptor
thrombin receptor
alpha-thrombin rec
hypothetical prote
probable TonB-depe
fusin (LESTRA) - c
neuropeptide Y/pep
probable transport
probable transport
thrombin receptor
G protein-coupled
olfactory channel
protein B0212.5 [i
heptahelical P2Y5-
bradykinin B1 rece
kappa opioid recep
opioid receptor ho
G protein-coupled
orphan opioid rece
hypothetical prote
phosphomannomutase
hypothetical prote
hypothetical prote
angiotensin recept
probable amino aci
hypothetical prote
probable ferredoxi
phosphomannomutase
probable RING zinc
G protein-coupled
probable sugar upt
bradykinin B1 rece
interleukin-8 rece
angiotensin II rec
ubiquinol-cytochro
bradykinin B2 rece
kappa opioid recep
kappa opioid recep
kappa opioid recep
kappa opioid recep
hypothetical prote
proteinase activat
probable integral
hypothetical prote
probable glycosyl
potassium-transport
potassium-transport
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
G protein-coupled
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
ubiquinol-cytochro
rhodopsin - giant
probable membrane
polyamine transport
hypothetical prote
G protein-coupled

chemokine (C-C) receptor 5 - human
N/Alternate names: C-C CKR-5; CCR5
C/Species: Homo sapiens (man)
C/Date: 12-Jul-1996 [Sequence revision 12-Jul-1996 #text change 20-Jun-2000
C/Accession: A43113; S71808; A58832; G02653; A58833
R/Sanson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A/Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A/Reference number: A43113; MUID:96241590; PMID:8639485
A/Accession: A43113
A/Molecule type: mRNA
A/Residues: 1-352 <SAM>
A/Cross-references: GB:X91492; NID:gl262810; PIDN:CAA62796.1; PID:gl262811
R/Sanson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liegnard, C.; Farber, C.M.; Saragost
M.; Imai, T.; Rana, S.; Ye, Y.; Smyth, R.D.; Collman, R.G.; Doms, R.W.; Vassart, G.; Par
Nature 382, 722-725, 1996
A/Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of
A/Reference number: S71808; MUID:96345670; PMID:8751444
A/Accession: S71808
A/A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 182-206;207-230 <SAM2>
A/Accession: A58834
A/A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-184; 'IKDSHLGAGPAAACHGELLGNPNKNSASVSK' <SAM3>
A/Cross-references: GB:X99393; NID:gl524062; PIDN:CAA67767.1; PID:gl524063
A/Note: this frameshift mutation results in a non-functional receptor but confers a degra
nd may have had a selective advantage by conferring resistance to Yersinia plague infect
R/Combadere, C.; Anujay, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A/Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec
A/Reference number: A58832; MUID:96295970; PMID:8699119
A/Accession: A58832
A/Molecule type: mRNA
A/Residues: 1-352 <COM1>
A/Cross-references: GB:U57840; NID:gl502408; PIDN:AAB17071.1; PID:gl502409
A/Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R/Combadere, C.
submitted to the EMBL Data Library, May 1996
A/Reference number: H01541
A/Accession: G02653
A/A>Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-89; 'L', 91-352 <COM2>
A/Cross-references: EMBL:U57840
R/Raport, C.J.; Goding, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A/Title: Molecular cloning and functional characterization of a novel human CC chemokine
A/Reference number: A58833; MUID:96291862; PMID:8663314
A/Accession: A58833
A/Molecule type: mRNA
A/Residues: 1-352 <CRAP>
A/Cross-references: GB:U54994; NID:gl457945; PIDN:AAC50598.1; PID:gl457946
C/Comment: This is a receptor for chemokines MIP-1alpha (see F1R:A30574), MIP-1beta (see
C/Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C
C) Genetics:
A/Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CCR5; ChemR13
A/Cross-references: GDB:I230510; OMIM:601373
A/Map position: 3p21-3p21
C/Function:
A/Note: probably acts to control granulocyte proliferation and differentiation
C/Superfamily: vertebrate rhodopsin
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran
F132-56/Domain: transmembrane #status predicted <TM1>
F132-56/Domain: transmembrane #status predicted <TM2>
F103-124/Domain: transmembrane #status predicted <TM3>

```

Query Match          100.0%; Score 126; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 QWDFGNTMCQLLTGLTYFIFGFSS 22
        |||||
DDB     93 QWDFGNTMCQLLTGLTYFIFGFSS 114
        |||||

RESULT 2
JC2443
chেমokine (C-C) receptor 2, splice form B - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte che
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C:CAccession: JC2443; I38463
C:R.Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant prot
A:Reference number: JC2443; MUID:94324942; PMID:8048929
A:CAccession: JC2443
A:Molecule type: mRNA
A:Residues: 1-360 <YMA>
A:Cross-references: DDBU:D29984; NID:g531246; PIDD:BAA06253.1; PID:g531247
A:Charo, R.R., Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant pr
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:CAccession: I38463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-360 <RES>
A:Cross-references: EMBL:U03905; NID:g472557; PIDD:AAA19120.1; PID:g472558
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F:13-70/Domain: transmembrane #status predicted <TM1>
F:781-100/Domain: transmembrane #status predicted <TM2>
F:F115-136/Domain: transmembrane #status predicted <TM3>
F:F154-178/Domain: transmembrane #status predicted <TM4>
F:F207-226/Domain: transmembrane #status predicted <TM5>
F:F244-268/Domain: transmembrane #status predicted <TM6>
F:287-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (asn) (covalent) #status predicted
F:113-190/Disulfide bonds: #status predicted

Query'Match          69.0%; Score 87; DB 2; Length 360;
Best Local Similarity 66.7%; Pred. No. 1.4e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY      1 QWDFGNTMCQLLTGLTYFIFGF 21
        :|||||:|:|||||:|:|
DDB     105 EWVFNAMCKLFTGLYHIGTF 125
        :|||||:|:|||||:|:|

RESULT 3
I38450
chেমokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte che
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text change 13-Aug-1999

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F:36-63/Domain: transmembrane #status predicted <TM1>
F:73-94/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:200-222/Domain: transmembrane #status predicted <TM5>
F:239-260/Domain: transmembrane #status predicted <TM6>
F:283-304/Domain: transmembrane #status predicted <TM7>

Query Match          65.1%; Score 82; DB 2; Length 355;
Best Local Similarity 54.5%; Pred. No. 7.9e-05;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      1 QWDFGNWCOLLTGLYFIGRFS 22
      ||| ||::||:|::||:|
Db       98 QWFGFTWCKVSGFYIGFYS 119

RESULT 5
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C:Species: Mus musculus (house mouse)
C:Title: Cloning and differential tissue-specific expression of three mouse beta chemokini
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49339
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokini
A:Reference number: I49339; MUID:95340546; PMID:7542241
C:Accession: I49339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C:Superfamily: vertebrate rhodopsin

Query Match          60.3%; Score 76; DB 2; Length 355;
Best Local Similarity 52.4%; Pred. No. 0.00065;
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY      2 WDFGNWCOLLTGLYFIGRFS 22
      ||| ||:|::||:|::|
Db       99 WIFGDAMCKLLSGFYILGLYS 119

RESULT 6
I49340
MIP-1 alpha receptor like-1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49340
R:Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokini
A:Reference number: I49339; MUID:95340546; PMID:7542241
C:Accession: I49340
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-356 <RES>
A:Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C:Superfamily: vertebrate rhodopsin

Query Match          58.7%; Score 74; DB 2; Length 356;
Best Local Similarity 47.6%; Pred. No. 0.0013;
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      2 WDFGNWCOLLTGLYFIGRFS 22
      ||| ||:|::||:|::|
Db       100 WIFGNAMCKVSGFYILGLYS 120

RESULT 7
A45177
chemokine (C-C) receptor 1 - human
N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

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C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: A45177; I55671
 R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-
 A:Reference number: A45177; MUID:93161416; PMID:7679328
 A:Accession: A45177
 A:Status: preliminary; functional expression, and signaling characteristics of a C-
 A:Molecule type: mRNA
 A:Residues: 1-355 <RES>
 A:Cross-references: GB:110918; NID:9292416; PIDN:AAA36543.1; PID:9292417
 A:Experimental source: H60 cells
 A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
 R:Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
 A:Reference number: I55671; MUID:93240122; PMID:7683036
 A:Accession: I55671
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-355 <RES>
 A:Cross-references: GB:110918; NID:9292416; PIDN:AAA36543.1; PID:9292417
 C:Genetics:
 A:Gene: GDB:CMKBR1; CMKBR-1
 A:Cross-references: GDB:1138446; OMIM:601159
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr
 F:108-129/Domain: transmembrane #status predicted <TM1>
 F:147-171/Domain: transmembrane #status predicted <TM3>
 F:205-223/Domain: transmembrane #status predicted <TM4>
 F:240-261/Domain: transmembrane #status predicted <TM5>
 F:288-305/Domain: transmembrane #status predicted <TM6>
 F:5/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:24-273,106-183/Disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 Query Match 56.3%; Score 71; DB 2; Length 355;
 Best Local Similarity 47.6%; Pred. No. 0.0038;
 Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 2 WDFGNTWCOLLTGLYFIFGFFS 22
 DB 99 WVFQNMCKILSGFYITGLYS 119
 RESULT 8
 I49341
 MIP-1 alpha receptor like-2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
 C:Accession: I49341
 R:Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
 A:Reference number: I49339; MUID:95340546; PMID:7542241
 A:Accession: I49341
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>
 A:Cross-references: EMBL:U28406; NID:9881551; PID:9881552
 C:Superfamily: vertebrate rhodopsin
 Query Match 55.6%; Score 70; DB 2; Length 359;
 Best Local Similarity 40.9%; Pred. No. 0.0054;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 QY 1 QWDFGNTWCOLLTGLYFIFGFFS 22
 DB 102 EWFGHYMKMLSGFYITGLYS 123

RESULT 9

G02436

chemokine (C-C) receptor 3 - human

N:Alternate names: C-C CKR-3

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000

C:Accession: G02436; A57237

R:Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A:Reference number: H01272

A:Accession: G02436

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <PON>

A:Cross-references: EMBL:U49727; NID:91477560; PIDN:AA09726.1; PID:91477561

R:Combadere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.

A:Reference number: A57237; MUID:95348056; PMID:7622448

A:Accession: A57237

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106, N', 108-275, S', 277-280, R', 282-355 <COM>

A:Cross-references: GB:U28694; NID:91199579; PIDN:AA050469.1; PID:91199580

A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AA050469.

C:Genetics:

A:Gene: GDB:CMKBR3

A:Cross-references: GDB:579624; OMIM:601268

A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F:36-60/Domain: transmembrane #status predicted <TM1>

F:71-91/Domain: transmembrane #status predicted <TM2>

F:108-129/Domain: transmembrane #status predicted <TM3>

F:147-171/Domain: transmembrane #status predicted <TM4>

F:205-223/Domain: transmembrane #status predicted <TM5>

F:240-261/Domain: transmembrane #status predicted <TM6>

F:288-305/Domain: transmembrane #status predicted <TM7>

F:24-273,106-183/Disulfide bonds: #status predicted

F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 53.2%; Score 67; DB 2; Length 355;
 Best Local Similarity 52.4%; Pred. No. 0.015;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 WDFGNTWCOLLTGLYFIFGFFS 22

DB 99 WVFQNMCKILSGFYITGLYS 119

RESULT 10

A57160

chemokine (C-C) receptor 4 - human

N:Alternate names: C-C CKR-4

C:Species: Homo sapiens (man)

C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

C:Accession: A57160

R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.L.; V

J. Biol. Chem. 270, 19495-19500, 1995

A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cl

A:Reference number: A57160; MUID:95370289; PMID:7642634

A:Accession: A57160

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-360 <POM>

A:Cross-references: GB:X85740; NID:91370103; PIDN:CAA59743.1; PID:9971452

C:Genetics:

A:Gene: GDB:CMKBR4

A:Cross-references: GDB:677463

A:Map position: 3p21-3p21

C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;40-65/Domain: transmembrane #status predicted <TM1>
 F;76-97/Domain: transmembrane #status predicted <TM2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;243-264/Domain: transmembrane #status predicted <TM6>
 F;291-308/Domain: transmembrane #status predicted <TM7>
 F;29-276,110-187/Disulfide Bonds: #status predicted
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 52.4%; Score 66; DB 2; Length 360;
 Best Local Similarity 40.9%; Pred. No. 0.022;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLTLGLYFIFGFS 22
 ||| :||: :||:
 Db 102 QWVFGGLCKLKWVWVYLVGFYS 123

RESULT 11
 JC5942
 Chemokine receptor - human
 C;Species: Homo sapiens (man)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: JC5942
 R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
 Biochem. Biophys. Res. Commun. 243, 264-268, 1998
 A;Title: Cloning and characterization of a novel human chemokine receptor.
 A;Reference number: JC5942; MUID:98139902; PMID:9473515
 A;Accession: JC5942
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-344 <PAN>
 A;Cross-references: GB:U97123; NID:G2897070; PIDN:AA039595.1; PID:G2897071
 C;Superfamily: vertebrate rhodopsin

Query Match 51.6%; Score 65; DB 2; Length 344;
 Best Local Similarity 55.6%; Pred. No. 0.03; Mismatches 5; Indels 0; Gaps 0;
 Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GNTMQLTLGLYFIFGFS 22
 ||| :||: :||:
 Db 99 GDPCKILILGLYFVGLYS 116

RESULT 12
 JC4587
 Chemokine (C-C) receptor 4 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C;Accession: JC4587
 R;Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A;Reference number: JC4587; MUID:96136324; PMID:8573157
 A;Accession: JC4587
 A;Molecule type: mRNA
 A;Residues: 1-360 <HOO>
 A;Cross-references: EMBL:X90862; NID:G1167851; PIDN:CAA62372.1; PID:G1167852
 A;Experimental source: thymus
 C;Genetics:
 A;Gene: cc ckr-4
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F;2,183,194/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 51.6%; Score 65; DB 2; Length 360;
 Best Local Similarity 40.9%; Pred. No. 0.031;
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLTLGLYFIFGFS 22
 ||| :||: :||:
 Db 102 QWVFGGLCKLKWVWVYLVGFYS 123

RESULT 13
 I58186
 probable G protein-coupled receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
 C;Accession: I58186
 R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
 Neurosci. Lett. 169, 85-89, 1994
 A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and
 A;Reference number: I58186; MUID:94323113; PMID:8047298
 A;Accession: I58186
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-354 <RES>
 A;Cross-references: EMBL:U04808; NID:G2558635; PIDN:AA887093.1; PID:G439861
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 47.6%; Score 60; DB 2; Length 354;
 Best Local Similarity 62.5%; Pred. No. 0.18;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 NTMQLTLGLYFIFGFS 21
 ||| :||: :||:
 Db 100 NAMCKLTTFATFFIGFF 115

RESULT 14
 JC5068
 G protein-coupled receptor CKR-L3 - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C;Accession: JC5068
 R;Zaballos, A.; Varona, R.; Guierres, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
 A;Reference number: JC5067; MUID:97040707; PMID:8886020
 A;Accession: JC5068
 A;Molecule type: DNA
 A;Residues: 1-369 <ZAB>
 A;Cross-references: EMBL:Z79784; NID:G1668737; PIDN:CA802144.1; PID:G1668738
 C;Comment: This protein belongs to the family of alpha chemokine receptors.
 C;Genetics:
 A;Gene: GDB:CMKBR6; STBL22; GPR29; CCR6; CKR-L3; GPR-CY4
 A;Cross-references: GDB:5370639; OMIM:601835
 A;Map position: 6q27-6q27
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein
 F;42-68/Domain: transmembrane #status predicted <TM1>
 F;79-99/Domain: transmembrane #status predicted <TM2>
 F;115-136/Domain: transmembrane #status predicted <TM3>
 F;160-180/Domain: transmembrane #status predicted <TM4>
 F;212-233/Domain: transmembrane #status predicted <TM5>
 F;250-271/Domain: transmembrane #status predicted <TM6>
 F;292-315/Domain: transmembrane #status predicted <TM7>

Query Match 46.8%; Score 59; DB 2; Length 369;
 Best Local Similarity 52.6%; Pred. No. 0.26;
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 WDFGNTMQLTLGLYFIFG 20
 ||| :||: :||:
 Db 106 WVFSNATCKLKGIVAINF 124

C>Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Jul-2000
 C/Accession: I38973
 R/O'Dowd, B.F.; Scheideler, M.A.; Nguyen, T.; Cheng, R.; Rasmussen, J.S.; Zastawny, R.;
 Genomics 28, 84-91, 1995
 A>Title: The cloning and chromosomal mapping of two novel human opioid-somatostatin-like
 A/Reference number: A57647; MUID:96070436; PMID:7590751
 A/Accession: I38973
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-328 <RES>
 A/Cross-references: EMBL:U22491; NID:9553232; PIDN:AA050197.1; PID:9553233
 C/Genetics:
 A/Gene: GDB:GPR7
 A/Cross-references: GDB:371714; OMIM:600730
 A/Map position: 10q11.2-10q21.1
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor

Query Match 42.5%; Score 53.5; DB 2; Length 328;
 Best Local Similarity 35.5%; Pred. No. 1.6;
 Matches 11; Conservative 4; Mismatches 7; Indels 9; Gaps 1;
 QY 1 QWDRGNTMCLL-----TGLYFIFGPF 22
 DB 101 QWDFGELMCKLVAIDQYNTFSYFLTVMS 131

RESULT 18
 A55735
 G protein-coupled receptor EB11 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
 C/Accession: A55735
 R/Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A>Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A/Reference number: A55735; MUID:95154835; PMID:7851893
 A/Accession: A55735
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-378 <SCH>
 A/Cross-references: GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor

Query Match 42.1%; Score 53; DB 2; Length 378;
 Best Local Similarity 42.9%; Pred. No. 2.2;
 Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 2 WDRGNTMCLLGLYFIFGPF 22
 DB 122 WIRGVYCKGIFGIYKLSF 142

RESULT 19
 JC7080
 melanin-concentrating hormone receptor [validated] - human
 N/Alternate names: MCHR; orphan somatostatin-like receptor 1 (SLC-1)
 C/Species: Homo sapiens (man)
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
 C/Accession: JC7080
 R/Shinomura, Y.; Mori, M.; Sugo, T.; Ishibashi, Y.; Abe, M.; Kurokawa, T.; Onda, H.; Ni;
 Biochem. Biophys. Res. Commun. 261, 622-626, 1999
 A>Title: Isolation and identification of melanin-concentrating hormone as the endogenous
 A/Reference number: JC7080; MUID:99373129; PMID:10441476
 A/Accession: JC7080
 A/Molecule type: mRNA
 A/Residues: 1-422 <SHI>
 A/Note: It is uncertain whether Met-1, Met-6 or Met-70 is the initiation codon
 C/Superfamily: neurokinin 1 receptor
 C/Keywords: hormone receptor; transmembrane protein

Query Match 42.1%; Score 53; DB 2; Length 422;
 Best Local Similarity 42.9%; Pred. No. 2.2;
 Matches 9; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 2 WDRGNTMCLLGLYFIFGPF 22
 DB 122 WIRGVYCKGIFGIYKLSF 142

RESULT 16
 S55594
 G protein-coupled receptor E1 - equine herpesvirus 2
 C/Species: equine herpesvirus 2
 C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C/Accession: S55594
 R/Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
 J. Mol. Biol. 249, 520-528, 1995
 A>Title: The DNA sequence of equine herpesvirus 2.
 A/Reference number: S55594; MUID:95302501; PMID:7783207
 A/Accession: S55594
 A/Status: preliminary; nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-383 <TEL>
 A/Cross-references: GB:U20824; NID:9695172; PIDN:AAC13788.1; PID:9695173
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor

Query Match 43.7%; Score 55; DB 2; Length 383;
 Best Local Similarity 38.1%; Pred. No. 1.1;
 Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;
 QY 2 WDRGNTMCLLGLYFIFGPF 22
 DB 138 WIRGVYCKGIFGIYKLSF 158

RESULT 17
 I38973
 G protein-coupled receptor 7 - human
 C/Species: Homo sapiens (man)

2 WDEGNTMCQLLTGLYFIFGFFS 22
122 WVEGVHFCFLIFAIYKMSFFS 142

RESULT 22
S27357

C:Accession: S27357
C:Author: R.P. Parrot, J.J. Raspe, E. Vassart, G. Parmentier, M.
C:Journal: J. Biol. Chem. J. 288, 911-917, 1992
C:Title: Cloning and functional expression of the canine anaphylatoxin C5a
C:Species: Canis lupus familiaris (dog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S27357

A;Residues: 1-352 <PER>
A;Cross-references: EMBL:X65860; NID:g878; PIDN:CAA46690.1; PID:g879
C;Function:

C: Superfamily: vertebrate rhodopsin
A: Description: mediates the inflammatory and chemotactic responses in *Escherichia coli*
C: Superfamily: glycoprotein, inflammation: polymorph

[illegible]

F63-72/Domain: intracellular #status predicted <TM2>
F73-95/Domain: transmembrane #status predicted <TM>
F796-111/Domain: extracellular #status predicted <EX2>
F112-133/Domain: transmembrane #status predicted <TM3>
F120-133/Domain: transmembrane #status predicted <TM2>

F1734-150/Domain: intracellular #status predicted <TM>
F1734-150/Domain: transmembrane #status predicted <EX3>
F176-208/Domain: extracellular #status predicted <TM>
F209-229/Domain: transmembrane #status predicted <IN3>
F230-244/Domain: intracellular #status predicted <TM>

Accession	Protein	Cellular location	Protein type
F1230-244/Domain1	Intracellular	#status predicted	
F1245-266/Domain1	Transmembrane	#status predicted	
F1267-285/Domain1	Extracellular	#status predicted	
F1267-285/Domain2	Extracellular	#status predicted	
F1267-285/Domain3	Extracellular	#status predicted	

```
F;286-309/Domain: transmembrane #status predicted <in>
F;310-352/Domain: intracellular #status predicted <in>
P;5/Binding site: carboxydrate (Asn) (covalent) #status predicted
```

Query Match	40.5%;	Score 51;	DB 1;	Length 352;
Best Local Similarity	33.3%;	Prod. No. 4.1;		
		Estimated	9.	Models
			0.	Gaps
			0.	

Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0

Qy 2 WDFGNTWCQLLTGLYFIFGFFS 22

Db 103 WPFGNACRIILPSLILLNNYA 123

RESULT 23
JN0821

G protein-coupled receptor type B - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000

C: Accession: JNU621
R: Matsunaka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A;Title: Identification of novel members of G-protein coupled receptor superfamily
A;Reference number: JN0621; MUID:93326166; PMID:8392843
A;Accession: JN0621

A;Molecule type: mRNA
A;Residues: 1-350 <MAT>
A;Cross-references: GB:S63848; NTD:G399710; PIDN:AAB27547.1; PID:G399711

A: Experimental source: tongue taste papillae
C: Comment: This protein is involved in modulating taste sensitivity or regeneration of taste buds.
C: Superfamily: vertebrate rhodopsin

C; Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
F; 42-66/Domain: transmembrane #status predicted <TM1>
F; 80-99/Domain: transmembrane #status predicted <TM2>

F:114-135/Domain: transmembrane #status predicted <TM3>
F:154-175/Domain: transmembrane #status predicted <TM4>

F;200-222/Domain: transmembrane #status predicted <TM5>
F;242-265/Domain: transmembrane #status predicted <TM6>
F;284-306/Domain: transmembrane #status predicted <TM7>
F;6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.7%; Score 50; DB 2; Length 350;
Best Local Similarity 38.1%; Pred. No. 5.8;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 WDFGNTMCQLLTGLYIFIGFFS 22
DB 105 WVLGKIMCKVTSALTNYFVS 125

RESULT 24
A48921
N;Alternate names: G-protein coupled receptor Gpcrl6
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: A48921; A53677; I49348; I55421; H48909; I53774
R;Caretto, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the
A;Reference number: A48921; MUID:94117014; PMID:8288247
A;Accession: A48921
A;Molecule type: DNA
A;Residues: 1-359 <CR>
A;Cross-references: GB:I23637; NID:G435093; PIDN:AAA39305.1; PID:G435094
R;Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
J. Biol. Chem. 269, 18263-18266, 1994
A;Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding
A;Reference number: A53677; MUID:94308043; PMID:7518426
A;Accession: A53677
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-359 <SUZ>
A;Cross-references: GB:I26549
A;Note: Sequence extracted from NCBI backbone (NCBIP:149812)
R;Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A;Reference number: 149348; MUID:95363183; PMID:7636264
A;Accession: I49348
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: EMBL:U31207; NID:G950174; PIDN:AAC52239.1; PID:G950175
R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 29355-29358, 1994
A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression
A;Reference number: I55421; MUID:95050766; PMID:7961909
A;Accession: I55421
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-359 <RE2>
A;Cross-references: GB:LI3239; NID:G293665; PIDN:AAA62109.1; PID:G293666
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 175-184, 1993
A;Title: Identification, chromosomal location, and genome organization of mammalian G-protein coupled receptor type B
A;Reference number: A48909; MUID:94116980; PMID:8288218
A;Accession: H48909
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 145-258 <WIL>
A;Cross-references: GB:LI20337; NID:G438800; PIDN:AAA16853.1; PID:G438801
R;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A;Title: Cloning of a cDNA encoding a mouse homologue of the interleukin-8 receptor.
A;Reference number: I53774; MUID:94252584; PMID:8194768
A;Accession: I53774
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-359 <RE3>
A;Cross-references: GB:DI7630; NID:G493671; PIDN:BAA04536.1; PID:G493672
C;Genetics:
A;Gene: IL8B
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;49-74/Domain: transmembrane #status predicted <TM1>
F;84-106/Domain: transmembrane #status predicted <TM2>
F;120-141/Domain: transmembrane #status predicted <TM3>
F;163-182/Domain: transmembrane #status predicted <TM4>
F;213-234/Domain: transmembrane #status predicted <TM5>
F;251-271/Domain: transmembrane #status predicted <TM6>
F;308-328/Domain: transmembrane #status predicted <TM7>

Query Match 39.7%; Score 50; DB 2; Length 359;
Best Local Similarity 33.3%; Pred. No. 6;
Matches 7; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 WDFGNTMCQLLTGLYIFIGFFS 22
DB 111 WTFGSTLCKIFSVKVFYS 131

RESULT 25
T37324
probable JNK-activating protein kinase (EC 2.7.1.-) JNK-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T37324
R;Kawasaki, M.; Hisamoto, N.; Iino, Y.; Yamamoto, M.; Ninomiya-Tsuji, J.; Matsumoto, K.
EMBO J. 18, 3604-3615, 1999
A;Title: A Caenorhabditis elegans JNK signal transduction pathway regulates coordinated
A;Reference number: Z21688; MUID:99321749; PMID:10393177
A;Accession: T37324
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-435 <KAW>
A;Cross-references: EMBL:AB024086; NID:G5668698; PIDN:BAA92641.1; PID:G5668699
C;Genetics:
A;Gene: jkk-1
C;Function:
A;Description: activation of JNK-1
A;Pathway: JNK signaling pathway
A;Note: JNK pathway functions in type-D GABAergic motor neurons and thereby modulates c
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; signal transduction

Query Match 39.7%; Score 50; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 7.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTMCQLLTGLY 16
DB 307 WSLGIVTVQLVTGLY 321

RESULT 26
T16256
hypothetical protein F35C8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Jan-2000
C;Accession: T16256
R;Xu, X.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F35C8.
A;Reference number: Z18486
A;Accession: T16256
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-448 <WUX>
A;Cross-references: EMBL:U40941; NID:G1072184; PID:G1072189; PIDN:AAA81711.1; CESP:F35C1
C;Genetics:

A:Gene: CBSP.F35C8.3
 A:Introns: 70/1; 97/1; 134/1; 162/3; 201/3; 253/3; 308/3; 362/3; 393/3; 413/3
 C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 39.7%; Score 50; DB 2; Length 448;
 Best Local Similarity 60.0%; Pred. NO. 7.5;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTMQLLTGLY 16
 |||:|:|:|:|:|:|
 Db 320 WSLGTVVQLTGLY 334

RESULT 27
 I51372
 angiotensin II receptor - turkey
 C:Species: Meleagris gallopavo (common turkey)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Nov-1999
 C:Accession: I51372; FN0449
 R:Murphy, T.J.; Nakamura, Y.; Takeuchi, K.; Alexander, R.W.
 Mol. Pharmacol. 44, 1-7, 1993
 A:Title: A cloned angiotensin receptor isoform from the turkey adrenal gland is pharmacologically distinct from the human angiotensin II (AT1) receptor partial cDNA
 A:Reference number: FN0449; MUID:93221469; PMID:7916599
 A:Accession: I51372
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-359 <MUR>
 A:Cross-references: GDB:G349735; PIDN:AAA03560.1; PID:G349736
 R:Carasia, R.V.; McIlroy, P.J.; Kowalski, K.I.; Tilly, J.L.
 Biochem. Biophys. Res. Commun. 191, 1073-1080, 1993
 A:Title: Isolation of turkey adrenocortical cell angiotensin II (AT1) receptor partial cDNA
 A:Reference number: FN0449; MUID:93221469; PMID:7916599
 A:Accession: FN0449
 A:Molecule type: mRNA
 A:Residues: 53-91, 'C', 93-162, 'SSFIIVY', 171-231 <CAR>
 A:Cross-references: GB:S58041; NID:G299373; PIDN:AAB26041.1; PID:G299374
 A:Experimental source: liver
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: glycoprotein; phosphoprotein; transmembrane protein
 F:53-64/Domain: intracellular #status predicted <INI>
 F:65-86/Domain: transmembrane #status predicted <TM1>
 F:87-102/Domain: extracellular #status predicted <EX1>
 F:103-124/Domain: transmembrane #status predicted <TM2>
 F:125-142/Domain: intracellular #status predicted <IN2>
 F:143-162/Domain: transmembrane #status predicted <TM3>
 F:163-192/Domain: extracellular #status predicted <EX2>
 F:193-214/Domain: transmembrane #status predicted <TM4>
 F:215-238/Domain: intracellular #status predicted <IN3>
 F:239-262/Domain: transmembrane #status predicted <TM5>
 F:263-274/Domain: extracellular #status predicted <EX3>
 F:275-291/Domain: transmembrane #status predicted <TM6>
 F:136/Binding site: phosphate (Ser) (covalent) #status predicted
 F:141,233/Binding site: phosphate (Thr) (covalent) #status predicted
 F:176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.3%; Score 49.5; DB 2; Length 359;
 Best Local Similarity 50.0%; Pred. NO. 7.1;
 Matches 9; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 QWDFGNTMQLLTGLY 17
 |||:|:|:|:|:|:|
 Db 93 QWFGNCLKLAGISF 110

RESULT 28
 B55733
 G protein-coupled receptor GPR2 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 26-Aug-1999
 C:Accession: B55733
 R:Marchese, A.; Docherty, J.M.; Nguyen, T.; Heiber, M.; Cheng, R.; Heng, H.H.Q.; Tsui, I.
 Genomics 23, 609-618, 1994
 A:Title: Cloning of human genes encoding novel G protein-coupled receptors.

A:Reference number: A55733; MUID:95154831; PMID:7851889
 A:Accession: B55733
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-354 <MAR>
 A:Cross-references: GB:U13667
 C:Genetics:
 A:Gene: GDB:GPR2
 A:Cross-references: GDB:371708; OMIM:600240
 A:Map position: 17q21.1-17q21.3
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor

Query Match 38.9%; Score 49; DB 2; Length 354;
 Best Local Similarity 36.8%; Pred. NO. 8.4;
 Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNTMQLLTGLYFIFG 20
 |||:|:|:|:|:|:|
 Db 98 WSLGSATCRTISGLYSASF 116

RESULT 29
 JE0349
 interferon-inducible protein 10 (IP-10) receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
 C:Accession: JE0349
 R:Tamaru, M.; Tomingaga, Y.; Yatsunami, K.; Narumi, S.
 Biochem. Biophys. Res. Commun. 251, 41-48, 1998
 A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its cDNA
 A:Reference number: JE0349; MUID:99009219; PMID:9790904
 A:Accession: JE0349
 A:Molecule type: mRNA
 A:Residues: 1-367 <TM>
 A:Cross-references: DBJ:AB003174; NID:93798731; PIDN:BAA34045.1; PID:93798732
 C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
 C:Superfamily: vertebrate rhodopsin

Query Match 38.9%; Score 49; DB 2; Length 367;
 Best Local Similarity 36.4%; Pred. NO. 8.7;
 Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIFG 22
 |||:|:|:|:|:|:|
 Db 115 QWFGPGLCKVAGALFNIFYA 136

RESULT 30
 A57510
 mu opioid receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
 C:Accession: A57510; I48665; S66513; I49300
 R:Kauffman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.; Magendzo, K.; Newman, D.; Tran, T.
 J. Biol. Chem. 270, 15877-15883, 1995
 A:Title: Characterization of the murine mu opioid receptor gene.
 A:Reference number: A57510; MUID:95318184; PMID:7797593
 A:Accession: A57510
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-398 <KAU>
 A:Cross-references: GB:U19380
 R:Min, B.H.; Augustin, L.B.; Felsheim, R.F.; Fuchs, J.A.; Loh, H.H.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994
 A:Title: Genomic structure analysis of promoter sequence of a mouse mu opioid receptor gene
 A:Reference number: I48665; MUID:94377496; PMID:8090773
 A:Accession: I48665
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-398 <RES>
 A:Cross-references: EMBL:U10561; NID:9555696; PIDN:AAB60673.1; PID:9565069
 R:Rossi, G.C.; Fan, Y.X.; Brown, G.P.; Pasternak, G.W.

Fri Mar 5 14:59:14 2004

FEBS Lett. 369, 192-196, 1995
A;Title: Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing
A;Reference number: I49300; MUID:95377399; PMID:7649256
A;Accession: S66513
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-398 <ROS>
A;Cross-references: EMBL:U26915; NID:gl055230; PID:AAA81170.1; PID:gl055231
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C;Genetics:
A;Gene: MOR-1
A;Introns: 95/2; 213/1; 396/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran

Query Match 38.9%; Score 49; DB 2; Length 398;
Best Local Similarity 28.6%; Pred. No. 9.5;
Matches 6; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 2 WDFGNTWCOLLGLYFGFFS 22
| | | | : : : :
Db 133 WFCNLIKIVISIDYNNMF 153

Search completed: March 4, 2004, 18:03:58
Job time : 13.2245 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 7.18367 Seconds
(without alignments)
159.465 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNTMCLLTGLYFGPFS 22

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	352	1	P56493 cercopithec
2	126	100.0	352	1	Q9tv42 cercopithec
3	126	100.0	352	1	Q9tv42 cercopithec
4	126	100.0	352	1	P56439 gorilla gor
5	126	100.0	352	1	P51681 homo sapien
6	126	100.0	352	1	Q97883 hyllobates l
7	126	100.0	352	1	Q95nc5 hyllobates m
8	126	100.0	352	1	Q95nc5 hyllobates s
9	126	100.0	352	1	P79436 macaca mula
10	126	100.0	352	1	P56440 pan troglod
11	126	100.0	352	1	P56441 papio hamad
12	126	100.0	352	1	Q97881 pongo pygma
13	126	100.0	352	1	Q97880 pygathrix b
14	126	100.0	352	1	Q97878 trachypithe
15	126	100.0	352	1	Q97879 trachypithe
16	126	100.0	352	1	P56484 mus musculu
17	89	70.6	353	1	P41597 homo sapien
18	87	69.0	374	1	O55193 rattus norv
19	86	68.3	373	1	O08556 rattus norv
20	84	66.7	354	1	P32229 swinepox vi
21	83	65.9	269	1	VC03 SPVKA
22	83	65.9	370	1	VK02 SPVKA
23	83	65.9	373	1	Q98520 swinepox vi
24	82	65.1	355	1	P51683 mus musculu
25	82	65.1	356	1	P51685 homo sapien
26	81	64.3	360	1	Q97665 macaca mula
27	80	63.5	354	1	O18793 macaca mula
28	79	62.7	358	1	P51682 mus musculu
29	76	60.3	355	1	Q92213 cavia porce
30	75	59.5	359	1	P51675 mus musculu
31	74	58.7	356	1	O54814 rattus norv
32	71	56.3	355	1	P51676 mus musculu
33	71	56.3	355	1	P32246 homo sapien
					P56482 macaca mula

34	70	55.6	359	1	CKR3_MOUSE
35	67	53.2	355	1	CKR3_HUMAN
36	66	52.4	342	1	CKR6_CERAE
37	66	52.4	360	1	CKR4_HUMAN
38	65	51.6	342	1	CKR6_HUMAN
39	65	51.6	342	1	CKR6_MACNE
40	65	51.6	342	1	CKR6_PANTR
41	65	51.6	343	1	CKR6_MACFA
42	65	51.6	343	1	CKR6_MACMU
43	65	51.6	360	1	CKR4_MOUSE
44	61	48.4	381	1	V03L_CAVUK
45	60	47.6	354	1	C3X1_MOUSE
46	60	47.6	354	1	C3X1_RAT
47	59	46.8	374	1	CKR6_HUMAN
48	59	46.8	384	1	CKD6_HUMAN
49	58	46.0	355	1	CKR3_CERAE
50	58	46.0	355	1	CKR3_MACMU
51	56	44.4	355	1	C3X1_HUMAN
52	56	44.4	395	1	GP44_HUMAN
53	55	43.7	362	1	CKR4_MOUSE
54	55	43.7	378	1	CKD6_MOUSE
55	55	43.7	382	1	GP44_MOUSE
56	54	42.9	357	1	CKR9_HUMAN
57	54	42.9	382	1	CKD6_RAT
58	53.5	42.5	328	1	GP7_HUMAN
59	53	42.1	360	1	MCRI_RAT
60	53	42.1	378	1	CKR7_MOUSE
61	53	42.1	388	1	MCRI_MACMU
62	53	42.1	422	1	MCRI_HUMAN
63	53	42.1	423	1	MCRI_MOUSE
64	52.5	41.7	146	1	GP7_MOUSE
65	52	41.3	368	1	CCR3_HUMAN
66	52	41.3	369	1	CKR9_MOUSE
67	52	41.3	370	1	OPRX_CAVPO
68	52	41.3	378	1	CKR7_HUMAN
69	51	40.5	352	1	C5AR_CANFA
70	51	40.5	367	1	CKR6_MOUSE
71	51	40.5	371	1	NY6R_RABIT
72	51	40.5	537	1	P2Y8_XENLA
73	50.5	40.1	520	1	NFF2_HUMAN
74	50	39.7	350	1	CKRB_BOVIN
75	50	39.7	350	1	CKRB_HUMAN
76	50	39.7	359	1	IL8E_MOUSE
77	50	39.7	371	1	NY6R_MOUSE
78	50	39.7	389	1	UR2R_HUMAN
79	49.5	39.3	359	1	AG2R_CHICK
80	49.5	39.3	359	1	AG2R_MELGA
81	49	38.9	349	1	IL8A_RAT
82	49	38.9	362	1	CKRA_HUMAN
83	49	38.9	367	1	CCR3_MOUSE
84	49	38.9	398	1	OPRM_MOUSE
85	49	38.9	425	1	PAR1_HUMAN
86	49	38.9	425	1	PAR1_PAPHA
87	49	38.9	428	1	PAR1_CRILLO
88	48.5	38.5	337	1	OPSK_MOUSE
89	48.5	38.5	383	1	CYB_CALCR
90	48	38.1	345	1	C5AR_CAVPO
91	48	38.1	352	1	CCR4_CERTO
92	48	38.1	352	1	CCR4_HUMAN
93	48	38.1	352	1	CCR4_MACFA
94	48	38.1	352	1	CCR4_MACMU
95	48	38.1	352	1	CCR4_PAPAN
96	48	38.1	382	1	CCR4_MOUSE
97	48	38.1	397	1	PAR2_RAT
98	48	38.1	409	1	YOE6_ECOLI
99	48	38.1	420	1	PAR1_XENLA
100	48	38.1	482	1	C3AR_HUMAN

ALIGNMENTS

RESULT 1

Fri Mar 5 14:59:14 2004

CCRS CERAE
ID CCR5 CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Korak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U83324; AAC51795.1; -;
CC EMBL; U83325; AAC51796.1; -;
CC EMBL; AB015944; BAA31328.1; -;
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DOMAIN 302 352 11 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

FT VARIANT 14 14 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52B690C72EC29A CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QMDPQNTMCQLLTGLYFIFGFS 22
DB 93 QMDPQNTMCQLLTGLYFIFGFS 114

RESULT 2
CCRS CERP
ID CCR5 CERP STANDARD; PRT; 352 AA.
AC Q9TV42;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5.
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=100;
RX MEDLINE=9933215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
Diop O., Rigoulet J., Barre-Sinoussi F., Fomesgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
carrier status in African nonhuman primates.";
RT AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF035222; AAD44015.1; -;
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 2 (POTENTIAL).
FT TRANSMEM 69 89 3 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 4 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 5 (POTENTIAL).
FT DOMAIN 167 198 6 (POTENTIAL).
FT TRANSMEM 199 218 7 (POTENTIAL).
FT DOMAIN 219 235 8 (POTENTIAL).
FT TRANSMEM 236 260 9 (POTENTIAL).
FT DOMAIN 261 277 10 (POTENTIAL).
FT TRANSMEM 278 301 11 (POTENTIAL).

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-11; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22
 DB 93 QWDFGNTMCLLTGLYFIFGFS 114

RESULT 3

CKR5 CERTO STANDARD; PRT; 352 AA.
 ID CKR5 CERTO 062744; 062745; 062746;
 AC 062743; 062744; 062745; 062746;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN Cercobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OS Cercobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecoidea.
 OC NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Isolate 079, 085, 087, and 089;
 RX MEDLINE=98321155; PubMed=9656999;
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
 RT "Primary HIV isolates use the CCR5 coreceptor from sooty mangabeys
 naturally infected in west Africa: a comparison of coreceptor usage
 of primary HIV-1, HIV-2, and SIVmac.";
 RL Virology 246:113-124 (1998).
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC EMBL; AF051902; AAC39830.1; -
 CC EMBL; AF051903; AAC39831.1; -
 CC EMBL; AF051904; AAC39832.1; -
 CC EMBL; AF051905; AAC39833.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsin.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsin.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 FT VARIANT 2 2 D -> E (IN ISOLATE 087).
 FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
 FT VARIANT 25 25 V -> G (IN ISOLATE 087).
 FT VARIANT 100 100 M -> K (IN ISOLATE 079).
 FT VARIANT 107 107 L -> V (IN ISOLATE 089).
 FT VARIANT 134 134 V -> G (IN ISOLATE 079).
 FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
 FT VARIANT 340 340 T -> I (IN ISOLATE 079).
 SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-11; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22
 DB 93 QWDFGNTMCLLTGLYFIFGFS 114

RESULT 4

CKR5 GORGO STANDARD; PRT; 352 AA.
 ID CKR5 GORGO 15-JUL-1998 (Rel. 36, Created)
 AC P56439;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN Gorilla gorilla gorilla (Lowland gorilla).
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OC NCBI_TaxID=9595;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharroon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Feilner S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 or send an email to license@isb-sib.ch).
 CC EMBL; AF005659; AAB62553.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsin.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsin.

DR PROSITE; P500237; G PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; P500262; G PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40515 MW; D056FCB9PE5EAC84 CRC64;
 Query Match 100.0%; Score 126; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QMDFGNTMCLLTGLYFIFGFS 22
 DB 93 QMDFGNTMCLLTGLYFIFGFS 114
 RESULT 5
 CCR5 HUMAN STANDARD; PRT; 352 AA.
 ID PS1681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
 AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
 AC O14708; O15538; Q9UPA4;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR5) (CCR-5) (CCR5)
 DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
 DE CCR5 OR CMKBR5.
 OS Homo sapiens (Human).
 GN Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE-96241590; PubMed=8639485;
 RX Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
 RT "Molecular cloning and functional expression of a novel human
 RT C-C chemokine receptor gene";
 RL Biochemistry 35:3362-3367(1996).
 [2]
 SEQUENCE FROM N.A.
 RX MEDLINE-96291862; PubMed=8663314;
 RX Report C.J., Goeling J., Schweichart V.L., Gray P.W., Charo I.F.;
 RT "Molecular cloning and functional characterization of a novel human
 RT C-C chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha";
 RL J. Biol. Chem. 271:17161-17166(1996).
 [3]
 SEQUENCE FROM N.A.
 RX MEDLINE-96295970; PubMed=8699119;
 RX Comandiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
 RT "Cloning and functional expression of CCR5, a human monocyte CC
 RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
 RT RANTES";
 RL J. Leukoc. Biol. 60:147-152(1996).
 [4]
 SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
 RA Porcel B.M., Dragan Y., Giacalone J., Fae A., Powell E.,
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
 RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 [5]
 SEQUENCE FROM N.A.
 RP MEDLINE-98001387; PubMed=9343222;
 RX Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses";
 RL J. Virol. 71:8642-8656(1997).
 [6]
 SEQUENCE FROM N.A., AND POLYMORPHISMS.
 RP MEDLINE-98022612; PubMed=9359654;
 RX Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RX Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 [7]
 SEQUENCE FROM N.A.
 RP MEDLINE-98049523; PubMed=9388201;
 RX Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 RT with 5'-end heterogeneity, dual promoter usage, and evidence for
 RT polymorphisms within the regulatory regions and noncoding exons";
 RL J. Biol. Chem. 272:30662-30671(1997).
 [8]
 SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RP Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
 RP Debre P.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 [9]
 SEQUENCE FROM N.A.
 RP Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 [10]
 CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE-96260017; PubMed=8649511;
 RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
 RA di Marzio P., Broderick S., Sutton R.E., Hill C.M., Davis C.B.,
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 RT HIV-1";
 RL Nature 381:661-666(1996).
 [11]
 CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RP MEDLINE-96260018; PubMed=8649512;
 RX Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 RT CC-CKR-5";
 RL Nature 381:667-673(1996).
 [12]
 SULFATION.
 RP MEDLINE-99189752; PubMed=10089882;
 RX Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RX Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 RT entry";
 RL Cell 96:667-676(1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and rantes and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or

DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. . ; TAS.
DR GO; GO:0006954; P-inflammatory response; TAS.
DR GO; GO:0007125; P-invasive growth; TAS.
DR GO; GO:0007203; P-phosphatidylinositol-4,5-bisphosphate hydro. . ; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
FT Polymorphism.
KW FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIGFES 22
|||||
DB 93 QWDFGNTMCLLTGLYFIGFES 114
|||||

RESULT 6

CD	CKRS_HYLLE	STANDARD;	PRT;	352 AA.
ID	A097883;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).			
GN	CKCR5 OR CMKR5.			
OS	Hylobates leucogynus (White-cheeked gibbon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hylobatiidae; Hylobates.			
XC	NCBI_TaxID=61853;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99416438; PubMed=10486970;			
RA	Zhang Y.-W., Ryder O.A., Zhang Y.-P.;			
RT	"Sequence evolution of the CKRS chemokine receptor gene in primates.";			
FL	Mol. Biol. Evol. 16:11145-1154(1999).			
CC	-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,			
CC	MIP-1-beta and RANTES and subsequently transduces a signal by			
CC	increasing the intracellular calcium ions level. May play a role			
CC	in the control of granulocytic lineage proliferation or			
CC	differentiation.			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			

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EMBL; AF075451; A019863.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
G-Protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).

Fri Mar 5 14:59:14 2004

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FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DOMAIN 302 352 11 (POTENTIAL).
FT DISULFID 101 178 12 (POTENTIAL).
FT MOD RES 3 3 13 (POTENTIAL).
FT MOD RES 10 10 14 (POTENTIAL).
FT MOD RES 14 14 15 (POTENTIAL).
SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 7
CKR5_HYLM L STANDARD; PRT; 352 AA.
AC Q95NC0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Hylobates moloch (Silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF177899; AAK43382.1; -.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DISULFID 101 178 12 (POTENTIAL).
FT MOD RES 3 3 13 (POTENTIAL).
FT MOD RES 10 10 14 (POTENTIAL).
FT MOD RES 14 14 15 (POTENTIAL).
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 8
CKR5_HYLS Y STANDARD; PRT; 352 AA.
AC Q95NC5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF177884; AAK43367.1; -.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).

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FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF58A CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCOLLGLYFIFGFFS 22
Db 93 QWDFGNTMCOLLGLYFIFGFFS 114

RESULT 9
CKR5 MACMU STANDARD; PRT; 352 AA.
AC P79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544; 9541, 9545;
[1] SEQUENCE FROM N.A.
RN SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239."
RL J. Virol. 71:2522-2527 (1997).
[2] SEQUENCE FROM N.A.
RN SPECIES=M.mulatta;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry."
RL J. Virol. 71:2705-2714 (1997).
[3] SEQUENCE FROM N.A.
RN SPECIES=M.mulatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
[4] SEQUENCE FROM N.A.
RN SPECIES=M.mulatta;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

```

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RT RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).
CC 1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
CC 1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
EMBL; U77672; AAC51109.1; -
EMBL; U73739; AAC51158.1; -
EMBL; U6762; AAC34132.1; -
EMBL; AF005660; AAB62554.1; -
EMBL; AF005661; AAB62555.1; -
EMBL; AF005662; AAB62556.1; -
DR InterPro; IPR00276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCOLLGLYFIFGFFS 22
Db 93 QWDFGNTMCOLLGLYFIFGFFS 114

RESULT 10
CKR5 PANTR STANDARD; PRT; 352 AA.
ID CKR5 PANTR
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

```


GN CCR5 OR CMKR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host.";
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005663; AAB62557.1; -
CC EMBL; U94329; AAB58446.1; -
CC EMBL; AF011542; AAB65742.1; -
CC EMBL; U97666; AAC51670.1; -
CC EMBL; AF011540; AAB65740.1; -
CC EMBL; U89797; AAC03717.1; -
CC EMBL; AF177894; AAK43377.1; -
CC InterPro: IPR000276; GPCR_Rhodop.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
FT CAREOXYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF. 1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. le-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCOLLTGLYFIIGFFS 22
DB 93 QWDFGNTMCOLLTGLYFIIGFFS 114

RESULT 11
CCRS PAPER
ID CCR5 PAPER STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRS).
GN CCR5 OR CMKR5.
OS Papio hamadryas (Hamadryas baboon), and
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 9555;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RX MEDLINE=99210133; PubMed=10195758;
RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RT "Species-specific changes in the CCR5 gene from African and Asian
RT nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=P.anubis;
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by


```

CC      increasing the intracellular calcium ions level. May play a role
CC      in the control of granulocytic lineage proliferation or
CC      differentiation.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AF005658; AAB62552.1; -
CC      DR EMBL; AF105287; AAD20556.1; -
CC      DR EMBL; AF105288; AAD20557.1; -
CC      DR EMBL; AF105289; AAD20558.1; -
CC      DR EMBL; AF105290; AAD20559.1; -
CC      DR EMBL; AF023452; AAC63830.1; -
CC      DR InterPro; IPR000276; GPCR_Rhodpsn.
CC      Pfam; PF00001; 7tm.1; 1.
CC      DR PRINTS; PR00237; GPCR_RHODPSN.
CC      DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC      DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
CC      KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC      FT DOMAIN 1 30
CC      FT EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 31 58
CC      FT DOMAIN 59 68
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 69 89
CC      FT DOMAIN 90 102
CC      FT EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 103 124
CC      FT DOMAIN 125 141
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 142 166
CC      FT EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 167 198
CC      FT DOMAIN 199 218
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 219 235
CC      FT DOMAIN 236 260
CC      FT TRANSMEM 261 277
CC      FT EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 278 301
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT DOMAIN 302 352
CC      FT BY SIMILARITY.
CC      FT DISULFID 101 178
CC      FT MOD RES 3 3
CC      FT MOD RES 10 10
CC      FT MOD RES 14 14
CC      FT MOD RES 15 15
CC      FT MOD RES 15 15
CC      FT CARBOHYD 268 268
CC      FT N-LINKED (GLCNAC...) (POTENTIAL).
CC      SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE8B2 CRC64;
CC
CC      Query Match 100.0%; Score 126; DB 1; Length 352;
CC      Best Local Similarity 100.0%; Pred. No. 1e-11; Indels 0; Gaps 0;
CC      Matches 22; Conservative 0; Mismatches 0;
CC
CC      QY 1 QWDFGNTMCQLLTGLYFIFGFPS 22
CC      Db 93 QWDFGNTMCQLLTGLYFIFGFPS 114
CC
CC      RESULT 12
CC      CKR5_PONPY STANDARD; PRT; 352 AA.
CC      AC O97881;
CC      DT 30-MAY-2000 (Rel. 39, Created)
CC      DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC      DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC      DE C-C chemokine receptor type 5 (C-CR-5) (CC-CR-5) (CCR-5) (CCR5).
CC      GN CCR5 OR CMKBR5.
CC      OS Pongo pygmaeus (Orangutan).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
CC      OC NCBI_TaxID=9600;
CC      RN [1]
CC      RP SEQUENCE FROM N.A.

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RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AF075446; AAD19858.1; -
CC      DR InterPro; IPR000276; GPCR_Rhodpsn.
CC      Pfam; PF00001; 7tm.1; 1.
CC      DR PRINTS; PR00237; GPCR_RHODPSN.
CC      DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC      DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
CC      KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC      FT DOMAIN 1 30
CC      FT EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 31 58
CC      FT DOMAIN 59 68
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 69 89
CC      FT DOMAIN 90 102
CC      FT EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 103 124
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 125 141
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 142 166
CC      FT EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 167 198
CC      FT DOMAIN 199 218
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 219 235
CC      FT DOMAIN 236 260
CC      FT TRANSMEM 261 277
CC      FT EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 278 301
CC      FT CYTOPLASMIC (POTENTIAL).
CC      FT DOMAIN 302 352
CC      FT BY SIMILARITY.
CC      FT DISULFID 101 178
CC      FT MOD RES 3 3
CC      FT MOD RES 10 10
CC      FT MOD RES 14 14
CC      FT MOD RES 15 15
CC      FT MOD RES 15 15
CC      FT SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;
CC
CC      Query Match 100.0%; Score 126; DB 1; Length 352;
CC      Best Local Similarity 100.0%; Pred. No. 1e-11; Indels 0; Gaps 0;
CC      Matches 22; Conservative 0; Mismatches 0;
CC
CC      QY 1 QWDFGNTMCQLLTGLYFIFGFPS 22
CC      Db 93 QWDFGNTMCQLLTGLYFIFGFPS 114
CC
CC      RESULT 13
CC      CKR5_PYGBI STANDARD; PRT; 352 AA.
CC      AC O97880;
CC      DT 30-MAY-2000 (Rel. 39, Created)
CC      DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC      DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC      DE C-C chemokine receptor type 5 (C-CR-5) (CC-CR-5) (CCR-5) (CCR5).
CC      GN CCR5 OR CMKBR5.
CC      OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
CC      OC Pygathrix.
CC      OC NCBI_TaxID=61621;
CC      RN [1]

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```

RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075445; AAD19857.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN RECP Fl.1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP Fl.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 1 30 1 (POTENTIAL).
CC FT TRANSMEM 31 58 1 (POTENTIAL).
CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 69 89 2 (POTENTIAL).
CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 103 124 3 (POTENTIAL).
CC FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 142 166 4 (POTENTIAL).
CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 199 218 5 (POTENTIAL).
CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 236 260 6 (POTENTIAL).
CC FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 278 301 7 (POTENTIAL).
CC FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 101 178 BY SIMILARITY.
CC FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
CC FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
CC FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
CC SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 14
ID_CKRS PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKRS.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=54133;

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RN SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075448; AAD19860.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN RECP Fl.1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP Fl.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 1 30 1 (POTENTIAL).
CC FT TRANSMEM 31 58 1 (POTENTIAL).
CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 69 89 2 (POTENTIAL).
CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 103 124 3 (POTENTIAL).
CC FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 142 166 4 (POTENTIAL).
CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 199 218 5 (POTENTIAL).
CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 236 260 6 (POTENTIAL).
CC FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 278 301 7 (POTENTIAL).
CC FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 101 178 BY SIMILARITY.
CC FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
CC FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
CC FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
CC SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B861 CRC64;
Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 15
ID_CKRS TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKRS.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.

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Trachypithecus.
NCBI_taxid=61618;
[1]
SEQUENCE FROM N.A.
MEDLINE=99416438; PubMed=10486970;
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol Biol. Evol. 16:1145-1154 (1999).
-|- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
-|- SUBCELLULAR LOCATION: Integral membrane protein.
-|- SIMILARITY: belongs to family 1 of G-protein coupled receptors.

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EMBL: AF075443; AAC19855.1; -
InterPro: IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm1.1;
PRINTS: PR00237; GPCRHDOPSN.
PROSITE: PS00237; G_PROTEIN_RECP_F1.1; 1.
PROSITE: PS50242; G_PROTEIN_RECP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 68 2 (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 90 102 3 (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 6 (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 7 (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
FT MOD RES 352 AA; 40509 MW; 4366F148D3A5938F CR64;
SQ
Query Match 100.0%; Score 126; DB 1; Length 352;
Best: Local Similarity 100.0%; Pred. No.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNDFGNWCOLLGLYFGFFS 22
DB 93 QNDFGNWCOLLGLYFGFFS 114

RESULT 17
CKR8 MOUSE
ID CKR8_MOUSE STANDARD; PRT; 353 AA.
AC P56484;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8) (CCR-8).
GN CC8 OR CMK8R OR TER1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=98334001; PubMed=9670926;
RA Zingoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storlazzi C.T.,
RA Sinigaglia F., D'Ambrosio D., O'Garra A., Robinson D., Rocchi M.,
RA Santoni A., Zlotnick A., Nepolitano M.;
RT "The chemokine receptor CCR8 is preferentially expressed in Th2 but
RT not Th1 cells.";
RL J. Immunol. 161:547-551(1998).
CC -!- FUNCTION: Receptor for the TCA-3 chemokine.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
DR EMBL; Z98206; CAB10896.1; --
DR EMBL; Z98205; CAB10895.1; --
DR EMBL; AF001277; AAC97598.1; --
DR MGD; MGI:1201402; Ccr8.
DR GO; GO:0016493; P:C-C chemokine receptor activity; IDA.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0006935; P:chemotaxis; IDA.
DR InterPro; IPR004068; CC 8 receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR01530; CHEMOKINER8.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECP FL 2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein.
RW DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 62 71 2 (POTENTIAL).
FT TRANSMEM 72 91 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 92 105 3 (POTENTIAL).
FT TRANSMEM 106 127 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 128 144 4 (POTENTIAL).
FT TRANSMEM 145 169 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 170 200 5 (POTENTIAL).
FT TRANSMEM 201 220 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 221 236 6 (POTENTIAL).
FT TRANSMEM 237 261 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 262 278 7 (POTENTIAL).
FT TRANSMEM 279 302 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 303 353 BY SIMILARITY.
FT DISULFID 8 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 8
SQ SEQUENCE 353 AA; 40045 MW; 31BC4B642CDB9AE5 CRC64;
Query Match 70.6%; Score 89; DB 1; Length 353;
Best Local Similarity 63.6%; Pred. No. 4e-06;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 QWEGNTWCQLLYLGYIFGFFS 22
DB 96 QWVFGTAMKVVSLGYIFGFFS 117
RESULT 18
CKR2_HUMAN

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ID ID CKR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN CCR2 OR CWKBR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195821; PubMed=8146186;
RA Charo I.F., Myers S.J., Herman A., Francis C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94324942; PubMed=8049929;
RA Yamagami S., Tokuda Y., Ishii K., Tanaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
RT chemoattractant protein 1 receptor.";
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97150864; PubMed=8995400;
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RT carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Guoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. AND VARIANTS ILE.64 AND GLU-355.
RA Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX MEDLINE=20501139; PubMed=11046064;
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RA Chakravarty L., Kolattukudy P.B.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RT region.";
RL J. Immunol. 165:5295-5303(2000).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P41597-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P41597-2; Sequence=VSP_001893;
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC

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	EML;	U03882	; AA19119.1; --		
CC	EMEL;	U03905	; AA19120.1; --		
DR	EMBL;	D29984	; BAA06253.1; --		
DR	EMBL;	D50924	; AAC51637.1; --		
DR	EMBL;	U80924	; AACS1636.1; --		
DR	EMBL;	U95626	; AAB57791.1; --		
DR	EMBL;	U95626	; AAB57792.1; --		
DR	EMBL;	A954580	; XANI6400.1; --		
DR	PfR;	I38450	; I38450.		
DR	PIR;	JC2443	; JC2443.		
DR	PDB;	1KAD	; 14-AUG-02.		
DR	PDB;	LKP1	; 23-JAN-02.		
DR	Genew;	HGNC:	1603; CCR2.		
DR	MIM;	601267	; -. ;		
DR	GO;	GO:0005887	; C:integral to plasma membrane; TAS.		
DR	GO;	GO:0005625	; C:soluble fraction; TAS.		
DR	GO;	GO:0004950	; P:chemokine receptor activity; TAS.		
DR	GO;	GO:0006960	; P:antimicrobial humoral response (sensu Inver. .); TAS.		
DR	GO;	GO:0004968	; P:cellular defense response; TAS.		
DR	GO;	GO:0006935	; P:chemotaxis; TAS.		
DR	GO;	GO:0007204	; P:cytosolic calcium ion concentration elevation; TAS.		
DR	GO;	GO:0007125	; P:inflammatory response; TAS.		
DR	GO;	GO:0007125	; P:invasive growth; TAS.		
DR	GO;	GO:0007259	; P:JAK-STAT cascade; TAS.		
DR	GO;	GO:0007194	; P:negative regulation of adenylate cyclase ac. . ; TAS.		
DR	InterPro;	IPRO00276	; GPCR_Rhodpen.		
DR	Ffam;	PF00001	; 7tm1_1; 1.		
DR	PRINTS;	PR00237	; GPGRHODPSN.		
DR	PROSITE;	PS00337	; G_PROTEIN_RECEP_Fl_1; 1.		
DR	PROSITE;	PS00462	; G_PROTEIN_RECEP_Fl_2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;				
KM	Polymorphism; Alternative splicing; 3D-structure.				
FT	DOMAIN	1	42		
FT	TRANSMEM	43	70		
FT	DOMAIN	71	80		
FT	TRANSMEM	81	100		
FT	DOMAIN	101	114		
FT	TRANSMEM	115	136		
FT	DOMAIN	137	153		
FT	TRANSMEM	154	178		
FT	DOMAIN	179	206		
FT	TRANSMEM	207	226		
FT	DOMAIN	227	243		
FT	TRANSMEM	244	268		
FT	DOMAIN	269	285		
FT	TRANSMEM	286	309		
FT	DOMAIN	310	374		
FT	CARBOHYD	14	14		
FT	MOD_RES	26	26		
FT	DISULFID	113	190		
FT	VARSPLIC	314	374		
FT	VARIANT	64	64		
FT	VARIANT	355	355		
FT	SEQUENCE	374 AA;	41914 MW; F865E0D39E74CF0F CRC64;		
SO					

Query Match 68.3%; Score 86; DB 1; Length 373;
Best Local Similarity 66.7%; Pred. No. 1.2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGF 21
Db 118 EWVFGNIMCKLFTGLYHIGVF 138

RESULT 20
ID CKR5 RAT STANDARD; PRT; 354 AA.
AC O08556;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN CCR5 OR CMKBR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=98334064; PubMed=9670989;
RA Speleiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA Berger M., Gebicke-Haerter P.J.;
RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and
RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RL J. Neurosci. Res. 53:16-28(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis";
RL J. Neuroimmunol. 86:1-12(1998).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: Y12009; AAC72737.1; -;
CC DR EMBL: U77350; AAC03243.1; -;
CC DR InterPro: IPR000276; GPCR_Rhodopsin.
CC DR Pfam: PF00001; 7tm.1; 1.
CC DR PRINTS: PR00237; GPCRHHODOPSIN.
CC DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
CC DR PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 33 60 1 (POTENTIAL).
CC FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 71 91 2 (POTENTIAL).
CC FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 105 126 3 (POTENTIAL).
CC FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 144 168 4 (POTENTIAL).
CC FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 201 220 5 (POTENTIAL).
CC FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 238 262 6 (POTENTIAL).
CC FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
CC

FT TRANSMEM 280 303 7 (POTENTIAL).
FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
FT DISULFID 103 180 BY SIMILARITY.
FT CARBOHYD 270 270 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AAAC868D CRC64;

Query Match 66.7%; Score 84; DB 1; Length 354;
Best Local Similarity 61.9%; Pred. No. 2.3e-05;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGF 21
Db 95 EWVFGNIMCKLFTGLYHIGVF 115

RESULT 21
ID VK02 SPVKA STANDARD; PRT; 269 AA.
AC P32229;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE G-protein coupled receptor homolog C3.
DE C3L.
GN C3L.
OS Swinepox virus (strain Kasza) (SPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirus.
OX NCBI_TaxID=10277;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94069924; PubMed=8249275;
RA Massung R.F., Jayarama V., Moyer R.W.;
RT "DNA sequence analysis of conserved and unique regions of swinepox
RT virus: identification of genetic elements supporting phenotypic
RT observations including a novel G protein-coupled receptor
RT homologue.";
RL Virology 197:511-528(1993).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L22013; AAC37868.1; -;
CC DR InterPro: IPR000276; GPCR_Rhodopsin.
CC DR Pfam: PF00001; 7tm.1; 1.
CC DR PRINTS: PR00237; GPCRHHODOPSIN.
CC DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
CC DR PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.
CC KW G-protein coupled receptor; Transmembrane.
CC SQ SEQUENCE 269 AA; 31509 MW; CE1A192CCAB999A3 CRC64;

Query Match 65.9%; Score 83; DB 1; Length 269;
Best Local Similarity 54.5%; Pred. No. 2.4e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGF 22
Db 20 QWTFGNILCKIMSLVLYVGF 41

RESULT 22
ID VK02 SPVKA STANDARD; PRT; 370 AA.
AC Q08520;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE G-protein coupled receptor homolog K2.
GN K2R.
OS Swinepox virus (strain Kasza) (SPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirus.
OX NCBI_TaxID=10277;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94069924; PubMed=8249275;
RA Massing R.F., Jayarama V., Moyer R.W.;
RT "DNA sequence analysis of conserved and unique regions of swinepox
RT virus: identification of genetic elements supporting phenotypic
RT observations including a novel G protein-coupled receptor
RT homologue.";
RT Virology 137:511-528(1993).
RL -!- FUNCTION: Putative chemokine receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; L21931; AAC37873.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 61
FT TRANSFEM 62 82
FT DOMAIN 83 94
FT TRANSFEM 95 115
FT DOMAIN 116 131
FT TRANSFEM 132 152
FT DOMAIN 153 171
FT TRANSFEM 172 192
FT DOMAIN 193 223
FT TRANSFEM 224 244
FT DOMAIN 245 265
FT TRANSFEM 266 286
FT DOMAIN 287 300
FT TRANSFEM 301 321
FT DOMAIN 322 370
FT CARBOHYD 6 6
FT CARBOHYD 51 51
FT SEQUENCE 370 AA; 43171 MW; 76D08613327B0CC0 C64;
SQ
Query Match 65.94; Score 83; DB 1; Length 370;
Best Local Similarity 54.54; Pred. No. 3.3e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 QWFGNMTCOLTGYTFGRFS 22
DB 121 QWFGNMTCOLTGYTFGRFS 142
RESULT 23
CKR2 MOUSE
ID -CKR2 MOUSE STANDARD; PRT; 373 AA.
AC P51683; O61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (JE/FIC receptor) (MCP-1 receptor).
GN CCR2 OR CMKBR2.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemottractant protein 1) and murine macrophage inflammatory protein
RT alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9.";
RT J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE=96216064; PubMed=8662823;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
RT the C-C chemokines JE and FIC.";
RL J. Biol. Chem. 271:11603-11606(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97026720; PubMed=8872898;
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA Post T.W., Gerard C., Dorf M.E.;
RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
RT transcriptase-polymerase chain reaction does not detect mRNA for the
RT KC or new MCP-1 receptor.";
RL J. Neurosci. Res. 45:382-391(1996).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U47035; AAC52453.1; -
CC EMBL; U51717; AAC52557.1; -
CC EMBL; U56819; AAC52784.1; -
CC MGD; MGI:106185; Ccr2.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0019955; F:cytokine binding; IPI.
CC GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
CC GO; GO:0030037; P:hemoiesis; IMP.
CC GO; GO:0006959; P:humoral immune response; IMP.
CC GO; GO:0006954; P:inflammatory response; IMP.
CC GO; GO:0030334; P:regulation of cell migration; IMP.
CC InterPro; IPR00276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN
CC PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55
FT TRANSFEM 56 83
FT DOMAIN 84 93
FT TRANSFEM 94 114
FT DOMAIN 115 127
FT TRANSFEM 128 149
FT DOMAIN 150 166
FT TRANSFEM 167 191
FT DOMAIN 192 213
FT TRANSFEM 220 239
FT DOMAIN 220 239

FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 257 281 6 (POTENTIAL).
 FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 299 322 7 (POTENTIAL).
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 FT CONFLICT 39 39 Y -> H (IN REF. 1).
 FT CONFLICT 184 184 A -> G (IN REF. 1).
 FT CONFLICT 264 264 V -> G (IN REF. 1).
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 65.9%; Score 83; DB 1; Length 373;
 Best Local Similarity 61.9%; Pred. No. 3.4e-05;
 Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGF 21
 DB 118 EWVFGNTWCQVFTGLYHIGVF 138

RESULT 24

CKR8_HUMAN STANDARD; PRT; 355 AA.
 ID CKR8_HUMAN
 AC P51685;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 8 (C-C CKR-8) (CCR-8) (GPR-CV6)
 DE (GPCR) (Chemokine receptor-like 1) (CKR-L1) (TER1) (CKMBRL2) (CC-
 DE chemokine receptor CHEMRL1).
 GN CKR8 OR CKR8B OR CKRL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97351133; PubMed=9207005;
 RA Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M.,
 RA Combadiere C., Modi M., Bonner T.I., Murphy P.M.;
 RT "Identification of CCR8: a human monocyte and thymus receptor for the
 CC chemokine I-309.";
 RL J. Exp. Med. 186:165-170 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98129363; PubMed=9469461;
 RA Goya I., Gutierrez J., Varona R., Kremer L., Zaballios A., Marquez G.;
 RT "Identification of CCR8 as the specific receptor for the human beta-
 RT chemokine I-309: cloning and molecular characterization of murine
 CCR8 as the receptor for TCA-3.";
 RL J. Immunol. 160:1975-1981 (1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=8886020;
 RA Zaballios A., Varona R., Gutierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97131825; PubMed=8977299;
 RA Samson M., Stordeur P., Labbe O., Soularue P., Vaseart G.,
 RA Parmentier M.;
 RT "Molecular cloning and chromosomal mapping of a novel human gene,
 RT ChemR1, expressed in T lymphocytes and polymorphonuclear cells and
 RT encoding a putative chemokine receptor.";
 RL Eur. J. Immunol. 26:3021-3028 (1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Nakajima T., Yoshida R., Harada S.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP LIGAND BINDING.

RX MEDLINE=98180363; PubMed=9521068;
 RA Bernardini G., Hedrick J., Sozzani S., Iulini W., Spinetti G.,
 RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
 RA Napolitano M.;
 RT "Identification of the CC chemokines TARC and macrophage inflammatory
 RT protein-1 beta as novel functional ligands for the CCR8 receptor.";
 RL Eur. J. Immunol. 28:582-588 (1998).
 CC !- FUNCTION: Receptor for the chemokines SCYAL1-309, SCYAL4/MIP-1-
 CC beta and SCYAL7/TARC. May regulate monocyte chemotaxis and thymic
 CC cell line apoptosis. Alternative coreceptor with CD4 for HIV-1
 CC infection.
 CC !- SUBCELLULAR LOCATION: Integral membrane protein.
 CC !- SIMILARITY: belongs to family 1 of G-protein coupled receptors.
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 DR EMBL; U45983; AAB61962.1; -;
 DR EMBL; U62556; AAB05542.1; -;
 DR EMBL; Z79782; CAB02142.1; -;
 DR EMBL; Y08456; CAA69712.1; -;
 DR EMBL; D49919; BAA23387.1; -;
 DR EMBL; AF005210; AAB62547.1; -;
 DR PIR; JC5067; JC5067.
 DR Genew; HGNC:1609; CCR8.
 DR MIM; 601834; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 DR GO; GO:0015026; F:coreceptor activity; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR004068; CC 8 receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR01530; CHEMOKINER8.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 36 63 1 (POTENTIAL).
 FT DOMAIN 64 73 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 74 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 202 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 203 222 5 (POTENTIAL).
 FT DOMAIN 223 238 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 239 263 6 (POTENTIAL).
 FT DOMAIN 264 280 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 281 304 7 (POTENTIAL).
 FT DOMAIN 305 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 SQ SEQUENCE 355 AA; 40844 MW; BC14A153CF695361 CRC64;
 Query Match 65.1%; Score 82; DB 1; Length 355;
 Best Local Similarity 54.5%; Pred. No. 4.5e-05;
 Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 QWDFGNTWCQLLTGLYFIFGF 22
 DB 98 QWVFGTWCWKVSGFYIGFYS 119

RESULT 25

```
CKR8 MACMU STANDARD; PRT; 356 AA.
AC 097665;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 8 (C-C CR-8) (CC-CKR-8) (CCR-8)
GN CKR8.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
  receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -|- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY44/MIP-1-
  beta and SCY17/TARC. May regulate monocyte chemotaxis and thymic
  cell line apoptosis (By similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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  or send an email to license@isb-sib.ch).
CC
EMBL: AF100205; AAC72403.1; -
DR InterPro: IPR004068; CC_8_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR01530; CHEMOKINER8.
DR PRINTS: PR0237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G PROTEIN RECP F1.1; 1.
DR PROSITE: PS0262; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 63 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 64 73 2 (POTENTIAL).
FT TRANSMEM 74 93 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 94 107 3 (POTENTIAL).
FT TRANSMEM 108 129 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 130 146 4 (POTENTIAL).
FT TRANSMEM 147 172 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 173 203 5 (POTENTIAL).
FT TRANSMEM 204 223 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 224 239 6 (POTENTIAL).
FT TRANSMEM 240 264 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 265 281 7 (POTENTIAL).
FT TRANSMEM 282 305 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 306 356 BY SIMILARITY.
FT DISULFID 106 184
SQ SEQUENCE 356 AA; 41210 MW; 1979628DEE44845B CRC64;
Query Match 65.1%; Score 82; DB 1; Length 356;
Best Local Similarity 54.5%; Pred. No. 4.6e-05;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 QWDFGNTWCOLLTGLYIGFFS 22
DB 98 QWVGTVNCKVSGFYIGFYS 119
```

RESULT 26

```
CKR2 MACMU STANDARD; PRT; 360 AA.
AC 018793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CR-2) (CC-CKR-2) (CCR2)
DE Monocyte chemoattractant protein 1 receptor (MCP-1-R).
GN CKR2 OR CMKRP2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
  receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -|- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
  Transduces a signal by increasing the intracellular calcium ions
  level.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
  Name=B;
  Event=Alternative splicing; Named isoforms=2;
  Name=A;
  IsoId=O18793-1; Sequence=Displayed;
  IsoId=O18793-2; Sequence=Not described;
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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  or send an email to license@isb-sib.ch).
CC
EMBL: AF013958; AAD11572.1; -
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN RECP F1.1; 1.
DR PROSITE: PS0262; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
  Alternative splicing.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 136 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC... (POTENTIAL).
FT MOD RES 26 26 SULFATION (BY SIMILARITY).
FT DISULFID 113 190 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FB9F CRC64;
Query Match 64.3%; Score 81; DB 1; Length 360;
Best Local Similarity 65.0%; Pred. No. 6.5e-05;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```

CC      1 QWDFGNTMCLLGLYFIFGF 20
CC      : ||| ||| ||| ||| ||| |||
CC      105 EWVFGNANCKLFTGLYHIGY 124

RESULT 27
CC      CRK5_MOUSE
CC      ID CRK5_MOUSE STANDARD; PRT: 354 AA.
CC      AC P51682; O35313; O35891; P97308; P97405; Q61867;
CC      DT 01-OCT-1996 (Rel. 34, Created)
CC      DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC      DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC      DE C-C chemokine receptor type 5 (C-C CRK-5) (CCR-5) (MIP-1
CC      alpha receptor).
CC      GN CCR5 OR CCR5.
CC      OS Mus musculus (Mouse).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC      OX NCBI_TaxID=10090;
CC      RN [1]
CC      RY SEQUENCE FROM N.A.
CC      RC STRAIN=129/SVJ; TISSUE=Spleen;
CC      RX MEDLINE=96205938; PubMed=8631787;
CC      RA Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
CC      RA Charo I.F.;
CC      RT "Molecular cloning and functional expression of murine JR (monocyte
CC      chemoattractant protein 1) and murine macrophage inflammatory protein
CC      1 alpha receptors: evidence for two closely linked C-C chemokine
CC      receptors on chromosome 9.";
CC      RL J. Biol. Chem. 271:7551-7558 (1996).
CC      RN [2]
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
CC      RX MEDLINE=96278910; PubMed=8662890;
CC      RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
CC      RT "Cloning and characterization of a novel murine macrophage
CC      inflammatory protein-1 alpha receptor.";
CC      RL J. Biol. Chem. 271:14445-14451 (1996).
CC      RN [3]
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=129/Ola;
CC      RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
CC      RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC      RN [4]
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
CC      RX MEDLINE=98001387; PubMed=9343222;
CC      RA Kubmann S.E., Platt E.J., Kozak S.L., Kabat D.;
CC      RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
CC      implicate specific amino acids in infections by simian and human
CC      immunodeficiency viruses.";
CC      RL J. Virol. 71:8642-8656 (1997).
CC      RN [5]
CC      RP SEQUENCE FROM N.A.
CC      RC STRAIN=129;
CC      RX MEDLINE=97404635; PubMed=9261347;
CC      RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharon M., Cen Y.H.,
CC      Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
CC      RT "Two distinct CCR5 domains can mediate coreceptor usage by human
CC      immunodeficiency virus type 1.";
CC      RL J. Virol. 71:6305-6314 (1997).
CC      RN [6]
CC      RP SEQUENCE FROM N.A.
CC      RA Guo B., Kuno K., Harada A., Matsushima K.;
CC      RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC      CC -|- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC      MIP-1-beta and RANTES and subsequently transduces a signal by
CC      increasing the intracellular calcium ions level.
CC      CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC      CC -|- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC      but not in nonhematopoietic cell lines.
CC      CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC      or send an email to license@sib-sib.ch).

CC      EMBL: U47036; AAC52454.1; -
CC      EMBL: X94151; CMA63867.1; -
CC      EMBL: U68565; AAB37273.1; -
CC      EMBL: U83327; AAC53386.1; -
CC      EMBL: AF022990; AAC53389.1; -
CC      EMBL: AF019772; AAB71183.1; -
CC      EMBL: D83648; BAA12024.1; -
CC      MGD: MGI:107182; Ccr5.
CC      GO: GO:0016493; F1C-C chemokine receptor activity; IDA.
CC      GO: GO:0006952; P: defense response; IMP.
CC      InterPro: IPR000276; GPCR_Rhodpsn.
CC      Pfam: PF00001; 7tm 1; 1.
CC      PRINTS: PR00237; GPCRHHODPSN.
CC      PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC      PROSITE: PS00282; G_PROTEIN_RECEP_F1_2; 1.
CC      G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
CC      DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 33 60 1 (POTENTIAL).
CC      FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 71 91 2 (POTENTIAL).
CC      FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 105 126 3 (POTENTIAL).
CC      FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 144 168 4 (POTENTIAL).
CC      FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 201 220 5 (POTENTIAL).
CC      FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
CC      FT TRANSMEM 238 252 6 (POTENTIAL).
CC      FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
CC      FT TRANSMEM 280 303 7 (POTENTIAL).
CC      FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
CC      FT DISULFID 103 180 BY SIMILARITY.
CC      FT CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
CC      FT VARIANT 11 11 I -> S.
CC      FT VARIANT 62 62 K -> R.
CC      FT VARIANT 66 66 V -> M.
CC      FT VARIANT 97 97 I -> V.
CC      FT VARIANT 109 109 V -> L.
CC      FT VARIANT 156 156 V -> A.
CC      FT VARIANT 160 160 P -> S.
CC      FT VARIANT 185 185 P -> L.
CC      FT VARIANT 213 213 I -> V.
CC      FT VARIANT 318 318 I -> M.
CC      FT VARIANT 337 337 V -> A.
CC      FT CONFLICT 3 3 F -> L (IN REF. 2).
CC      FT CONFLICT 80 80 L -> P (IN REF. 2).
CC      FT CONFLICT 145 145 N -> I (IN REF. 5).
CC      FT CONFLICT 190 190 H -> Y (IN REF. 3).
CC      FT CONFLICT 208 208 P -> S (IN REF. 1).
CC      SQ SEQUENCE 354 AA; 40863 MW; B4AGB942E88F9CF0 CRC64;

Query Match 53.5%; Score 80; DB 1; Length 354;
Best Local Similarity 57.1%; Pred. No. 9.1e-05;
Matches 12; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLGLYFIFGF 21
DB 95 EWVFGNANCKLFTGLYHIGY 115

RESULT 28
CC      CRK3_CAVPO
CC      ID CRK3_CAVPO STANDARD; PRT: 358 AA.
CC      AC Q92213;

```

RESULT 29

DR GO: GO:0016493; F:C-C chemokine receptor activity; IDA.
 DR GO: GO:0005515; P:protein binding; IPI.
 DR GO: GO:0030595; P:immune cell chemotaxis; IDA.
 DR GO: GO:0006954; P:inflammatory response; IMP.
 DR GO: GO:0030099; P:myeloid blood cell differentiation; IMP.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm 1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN
 DR PROSITE: PS00237; G-PROTEIN RECP F1_1; 1.
 DR PROSITE: PS0262; G-PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 34
 FT TRANSMEM 35 60
 FT DOMAIN 61 64
 FT TRANSMEM 65 91
 FT DOMAIN 92 107
 FT TRANSMEM 108 129
 FT DOMAIN 130 146
 FT TRANSMEM 147 171
 FT DOMAIN 172 197
 FT TRANSMEM 198 223
 FT DOMAIN 224 239
 FT TRANSMEM 240 264
 FT DOMAIN 265 281
 FT TRANSMEM 282 305
 FT DOMAIN 306 355
 FT DISULFID 106 183
 FT CONFLICT 55 55 M -> V (IN REF. 2 AND 3).
 FT CONFLICT 149 149 L -> F (IN REF. 3).
 FT CONFLICT 278 278 H -> Q (IN REF. 3).
 SQ SEQUENCE 355 AA; 40901 MW; FCE9PFF70E6F38B1 CRC64;
 Query Match 60.3%; Score 76; DB 1; Length 355;
 Best Local Similarity 52.4%; Pred. No. 0.00037;
 Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 2 WDFGNTMCQLLTGLYFIFGFFS 22
 DB 99 WIFGDAMCKLISGFYILGLYS 119
 RESULT 30
 CCR3 RAT STANDARD; PRT; 359 AA.
 AC Q54814; 055169;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
 DE (CCR3).
 GN CCR3 OR CCKBR3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN-Wistar; TISSUE=Spleen;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
 RA Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Wistar; TISSUE=Spleen;
 RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
 RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
 CC microglia.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF003954; AAC03337.1; -.
 CC EMBL: Y13400; CAA73830.1; -.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm 1; 1.
 CC PRINTS: PR00237; GPCRHOPOPSN
 CC PROSITE: PS00237; G-PROTEIN RECP F1_1; 1.
 CC PROSITE: PS0262; G-PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 43
 FT TRANSMEM 44 64
 FT DOMAIN 65 74
 FT TRANSMEM 75 95
 FT DOMAIN 96 112
 FT TRANSMEM 113 133
 FT DOMAIN 134 154
 FT TRANSMEM 155 175
 FT DOMAIN 176 206
 FT TRANSMEM 207 227
 FT DOMAIN 228 243
 FT TRANSMEM 244 264
 FT DOMAIN 265 288
 FT TRANSMEM 289 309
 FT DOMAIN 310 359
 FT CONFLICT 164 164 P -> L (IN REF. 2).
 SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;
 Query Match 59.5%; Score 75; DB 1; Length 359;
 Best Local Similarity 45.5%; Pred. No. 0.00052;
 Matches 10; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
 DB 102 EWGFGHCCKMLSGLYLYLYS 123
 Search completed: March 4, 2004, 18:00:03
 Job time : 8.38367 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 35.4694 Seconds
(without alignments)
195.701 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNTMCQLLTGLYFIFGFFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

SPTREMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	126	100.0	215	4	O75303 homo sapien
2	126	100.0	333	4	O14694 homo sapien
3	126	100.0	339	4	Q9UN24 homo sapien
4	126	100.0	339	4	Q9UN23 homo sapien
5	126	100.0	339	4	Q9UBJ7 homo sapien
6	126	100.0	339	4	Q9UN25 homo sapien
7	126	100.0	339	4	Q9UN27 homo sapien
8	126	100.0	339	4	Q9UBT9 homo sapien
9	126	100.0	339	4	Q9UN28 homo sapien
10	126	100.0	339	6	Q9TQW0 hylobates c
11	126	100.0	339	6	Q9TUX1 hylobates c
12	126	100.0	339	6	Q9TUX8 gorilla gor
13	126	100.0	339	6	Q9TUT4 macaca neme
14	126	100.0	339	6	Q9TUT9 hylobates c
15	126	100.0	339	6	Q9TUD8 cercopithec
16	126	100.0	339	6	Q9TQW4 pan troglod

17	126	100.0	339	6	Q9TUM4	Q8tuw4 pan troglod
18	126	100.0	339	6	Q9TQU7	Q8tuq7 cercopithec
19	126	100.0	339	6	Q9TUU3	Q8tu3 macaca mula
20	126	100.0	339	6	Q9TUR3	Q8tur9 saginus sp
21	126	100.0	339	6	Q9TQT0	Q8tqt0 macaca fasc
22	126	100.0	339	6	Q9TUT9	Q8tut9 macaca mula
23	126	100.0	339	6	Q9TSN2	Q8tsn2 macaca fasc
24	126	100.0	339	6	Q9TSN6	Q8tsn6 cercopithec
25	126	100.0	339	6	Q9TQV6	Q8tqv6 colobus gue
26	126	100.0	339	6	Q9TUM6	Q8tuw6 pan troglod
27	126	100.0	339	6	Q9TQU9	Q8tuq9 cercopithec
28	126	100.0	339	6	Q9TSN3	Q8tsn3 macaca fasc
29	126	100.0	339	6	Q9TUU7	Q8tuu7 macaca fusc
30	126	100.0	339	6	Q9TQV0	Q8tqv0 papio papio
31	126	100.0	339	6	Q9TQU5	Q8tuq5 cercopithec
32	126	100.0	339	6	Q9TUS7	Q8tus7 papio papio
33	126	100.0	339	6	Q9TUT7	Q8tut7 pan troglod
34	126	100.0	339	6	Q9TUM3	Q8tuw3 pongo pygma
35	126	100.0	339	6	Q9TUS5	Q8tus5 papio papio
36	126	100.0	339	6	Q9TUU0	Q8tuu0 macaca mula
37	126	100.0	339	6	Q9TQV2	Q8tqv2 papio papio
38	126	100.0	339	6	Q9TQV3	Q8tqv3 cercopithec
39	126	100.0	339	6	Q9TQO8	Q8tuq8 cercopithec
40	126	100.0	339	6	Q9TQW2	Q8tqw2 pongo pygma
41	126	100.0	339	6	Q9TUU1	Q8tuu1 macaca mula
42	126	100.0	339	6	Q9TUT6	Q8tut6 macaca neme
43	126	100.0	339	6	Q9TSQ4	Q8tsq4 cercopithec
44	126	100.0	339	6	Q9TUT3	Q8tut3 macaca neme
45	126	100.0	339	6	Q9TUT0	Q8tut0 macaca neme
46	126	100.0	339	6	Q9TQR2	Q8tqr2 gorilla gor
47	126	100.0	339	6	Q9TUT8	Q8tut8 macaca mula
48	126	100.0	339	6	Q9TUT1	Q8tut1 macaca neme
49	126	100.0	339	6	Q9TUR0	Q8tur0 cercopithec
50	126	100.0	339	6	Q9TUM5	Q8tuw5 pan troglod
51	126	100.0	339	6	Q9TUS3	Q8tus3 lemur catta
52	126	100.0	339	6	Q9TQT2	Q8tqt2 macaca neme
53	126	100.0	339	6	Q9TQT1	Q8tqt1 macaca mula
54	126	100.0	339	6	Q9TUT5	Q8tut5 macaca neme
55	126	100.0	339	6	Q9TUT2	Q8tut2 macaca neme
56	126	100.0	339	6	Q9TUS8	Q8tus8 papio papio
57	126	100.0	339	6	Q9TUU4	Q8tuu4 macaca mula
58	126	100.0	339	6	Q9TUS6	Q8tus6 papio papio
59	126	100.0	339	6	Q9TUR7	Q8tur7 cercopithec
60	126	100.0	339	6	Q9TQU4	Q8tuq4 cercopithec
61	126	100.0	339	6	Q9TUT7	Q8tut7 macaca mula
62	126	100.0	339	6	Q9TUX0	Q8tux0 hylobates c
63	126	100.0	339	6	Q9TUU5	Q8tuu5 macaca fusc
64	126	100.0	339	6	Q9TUT1	Q8tut1 cercopithec
65	126	100.0	339	6	Q9TUS9	Q8tus9 papio papio
66	126	100.0	340	6	Q9TUU2	Q8tuu2 macaca mula
67	126	100.0	344	6	Q9TQR8	Q8tqr8 cercocebus
68	126	100.0	344	6	O77833	O77833 cercocebus
69	126	100.0	352	6	Q9TSK1	Q8tsk1 cercopithec
70	126	100.0	352	6	Q9SNC5	Q9snc5 hylobates s
71	126	100.0	352	6	Q9TV48	Q9tv48 cercopithec
72	126	100.0	352	6	Q9TV49	Q9tv49 cercocebus
73	126	100.0	352	6	Q9XT14	Q9xt14 colobus gue
74	126	100.0	352	6	O18771	O18771 pan troglod
75	126	100.0	352	6	Q9TV47	Q9tv47 cercopithec
76	126	100.0	352	6	Q9SNC1	Q9snc1 theropithec
77	126	100.0	352	6	O18770	O18770 pan troglod
78	126	100.0	352	6	O18772	O18772 pan troglod
79	126	100.0	352	6	Q9SNC6	Q9snc6 trachypithe
80	126	100.0	352	6	Q9SNC8	Q9snc8 colobus pol
81	126	100.0	352	6	Q9SNC0	Q9snc0 hylobates m
82	126	100.0	352	6	Q9SNC5	Q9snc5 cercopithec
83	126	100.0	352	6	Q9SNC5	Q9snc5 macaca arct
84	126	100.0	352	6	Q9XT12	Q9xt12 cercopithec
85	126	100.0	352	6	Q9TV42	Q9tv42 cercopithec
86	126	100.0	352	6	Q9XT13	Q9xt13 papio anubi
87	126	100.0	352	6	O77776	O77776 cercocebus
88	126	100.0	352	6	Q9MZA3	Q9mza3 hylobates a
89	126	100.0	352	6	Q9TV46	Q9tv46 cercopithec

90 126 100.0 352 6 Q9TSQ7
 91 126 100.0 352 6 Q9MZA2
 92 126 100.0 352 6 Q9TV50
 93 126 100.0 352 6 Q9XS99
 94 126 100.0 352 6 Q9TV45
 95 126 100.0 352 6 Q9SNE1
 96 126 100.0 352 6 Q9TV43
 97 126 100.0 352 6 Q9TV43
 98 126 100.0 352 6 Q9SNE8
 99 126 100.0 352 6 Q9TV46
 100 122 96.8 339 6 Q9TV46

ALIGNMENTS

RESULT 1
 O75303
 ID O75303 PRELIMINARY; PRT; 215 AA.
 AC O75303;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CC-chemokine receptor.
 GN CCR-5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tse L., Ehrenberg P.K., Chang G., Michael N.L.;
 RT "Genomic Organization and Functional Characterization of the Complete
 Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-
 Receptor for HIV-1.";
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF009962; AAC23944.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 215 AA; 23946 MW; 3C9146C768A416F7 CRC64;
 Query Match 100.0%; Score 126; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. NO. 1.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCOQLTGLYFIGFFS 22
 DB 93 QWDFGNTMCOQLTGLYFIGFFS 114
 RESULT 2
 O14694
 ID O14694 PRELIMINARY; PRT; 333 AA.
 AC O14694;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CCR5 receptor (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 Ho D.D.;
 RA "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
 RT AIDS Res. Hum. Retroviruses 0:0-0(1997).
 RL EMBL; AF011504; AAB65704.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 333 333
 SQ SEQUENCE 333 AA; 38174 MW; AEFBA07AG7893ABE CRC64;
 Query Match 100.0%; Score 126; DB 4; Length 333;
 Best Local Similarity 100.0%; Pred. NO. 3e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCOQLTGLYFIGFFS 22
 DB 74 QWDFGNTMCOQLTGLYFIGFFS 95
 RESULT 3
 Q9UN24
 ID Q9UN24 PRELIMINARY; PRT; 339 AA.
 AC Q9UN24;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 Shabata R., Yoder A., Pillai S., Kuiken C., Marx P., Molinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161919; AAD47676.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm1.1;
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;
 Query Match 100.0%; Score 126; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. NO. 3.1e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QWDFGNTMCOQLTGLYFIGFFS 22
 DB 86 QWDFGNTMCOQLTGLYFIGFFS 107
 RESULT 4
 Q9UN23

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ID Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 5
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
ID Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 5
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
ID Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
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KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 9C3369FF1F2F27A CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 6
Q9UN25 PRELIMINARY; PRT; 339 AA.
ID Q9UN25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161918; AAD47675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 7
Q9UN27 PRELIMINARY; PRT; 339 AA.
ID Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RA Kunzman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CBAEC2 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 8
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunzman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CBAEC2 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 9
Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunzman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6B1A6 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 10
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunzman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.

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DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAP2614D35C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 11
Q9TUX1 ID Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
[1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF161887; AAD47644.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257BFB834C4AE CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 12
Q9TUX8 ID Q9TUX8 PRELIMINARY; PRT; 339 AA.
AC Q9TUX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.

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OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
[1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF161894; AAD47651.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 13
Q9TUT4 ID Q9TUT4 PRELIMINARY; PRT; 339 AA.
AC Q9TUT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
[1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF161979; AAD47734.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548B0703C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 14
QSTUW9
ID Q9TUW9 PRELIMINARY; PRT; 339 AA.
AC Q9TUW9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor protein signalin.; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor protein signalin.; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
FT SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;
SQ
Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 15
QSTUW8
ID Q9TUW8 PRELIMINARY; PRT; 339 AA.
AC Q9TUW8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 16
QSTUW4
ID Q9TUW4 PRELIMINARY; PRT; 339 AA.
AC Q9TUW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor protein signalin.; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
FT SEQUENCE 339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;
SQ
Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 86 QWDFGNTMCQLLTGLYFIFGFS 107

RESULT 17
QSTUW4
ID Q9TUW4 PRELIMINARY; PRT; 339 AA.
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AC Q9TUM4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39159 MW; 8E699E882BAC0E84 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNWTCQLLTGLYFIQFFS 22
Db [1]
86 QWDFGNWTCQLLTGLYFIQFFS 107

RESULT 18
Q9TQV7
ID Q9TQV7 PRELIMINARY; PRT; 339 AA.
AC Q9TQV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

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DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNWTCQLLTGLYFIQFFS 22
Db [1]
86 QWDFGNWTCQLLTGLYFIQFFS 107

RESULT 19
Q9TUT3
ID Q9TUT3 PRELIMINARY; PRT; 339 AA.
AC Q9TUT3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161961; AAD47716.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39121 MW; AFB6E3EE4D6D3484 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNWTCQLLTGLYFIQFFS 22
Db [1]
86 QWDFGNWTCQLLTGLYFIQFFS 107

RESULT 20
Q9TUR9
ID Q9TUR9 PRELIMINARY; PRT; 339 AA.
AC Q9TUR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Saginus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=100754;

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RN 11
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD4770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
FT NON TER 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIIGFFS 22
Db 86 QWDFGNTMQLLTGLYFIIGFFS 107

RESULT 21
Q9TQT0 ID Q9TQT0 PRELIMINARY; PRT; 339 AA.
AC Q9TQT0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD4770.1; -.
DR EMBL; AF161950; AAD4770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
FT NON TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIIGFFS 22
Db 86 QWDFGNTMQLLTGLYFIIGFFS 107

RESULT 21
Q9TQT0 ID Q9TQT0 PRELIMINARY; PRT; 339 AA.
AC Q9TQT0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD4770.1; -.
DR EMBL; AF161950; AAD4770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
FT NON TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIIGFFS 22
Db 86 QWDFGNTMQLLTGLYFIIGFFS 107

RESULT 21
Q9TQT0 ID Q9TQT0 PRELIMINARY; PRT; 339 AA.
AC Q9TQT0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD4770.1; -.
DR EMBL; AF1616021; C:integral to membrane; IEA.

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QY 1 QWDFGNTMQLLTGLYFIIGFFS 22
Db 86 QWDFGNTMQLLTGLYFIIGFFS 107

RESULT 22
Q9TUT9 ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161972; AAD4772.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
FT NON TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCB5BA96C2F9E CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIIGFFS 22
Db 86 QWDFGNTMQLLTGLYFIIGFFS 107

RESULT 23
Q9TSN2 ID Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD4770.1; -.
DR EMBL; AF1616021; C:integral to membrane; IEA.

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DR GO: 0004872; P:receptor activity; IEA.
DR GO: 0001584; P:rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39137 MW; 95626ED3288607C1 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 24
Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Carciphithicus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO: 0001584; P:rhodopsin-like receptor activity; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39178 MW; 9DF2A6F446C5AED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 25
Q9TQV6 PRELIMINARY; PRT; 339 AA.
AC Q9TQV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -.
DR EMBL; AF162000; AAD47755.1; -.
DR EMBL; AF162001; AAD47756.1; -.
DR EMBL; AF162002; AAD47757.1; -.
DR EMBL; AF162003; AAD47758.1; -.
DR EMBL; AF162004; AAD47759.1; -.
DR GO: 0001584; P:rhodopsin-like receptor activity; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 26
Q9TQW6 PRELIMINARY; PRT; 339 AA.
AC Q9TQW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161900; AAD47657.1; -.
DR GO: 0001584; P:rhodopsin-like receptor activity; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

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DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5A4 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIFGFS 22
Db 86 QWDFGNTMCLLTGLYFIFGFS 107

RESULT 27
Q9TUQ9
ID Q9TUQ9 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5
OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162041; AAD47796.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF1F3ED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIFGFS 22
Db 86 QWDFGNTMCLLTGLYFIFGFS 107

RESULT 28
Q9TSN3
ID Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.

OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161951; AAD47707.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 35098 MW; F0132E8BC44EF829 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIFGFS 22
Db 86 QWDFGNTMCLLTGLYFIFGFS 107

RESULT 29
Q9TUU7
ID Q9TUU7 PRELIMINARY; PRT; 339 AA.
AC Q9TUU7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161955; AAD47711.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39037 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIFGFS 22

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DB      86 QWDFGNTWCQLLTGLYFICGFFS 107
|||||
RESULT 30
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
CX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161989; AAD47744.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39113 MW; 7F9803EA0E0AF9ED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFICGFFS 22
|||||
DB 86 QWDFGNTWCQLLTGLYFICGFFS 107

Search completed: March 4, 2004, 18:02:55
Job time : 36.4694 secs
```


ALIGNMENTS

RESULT 1
US-08-833-752-4
; Sequence 4, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-752-4

Query Match 100.0%; Score 126; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114
RESULT 2
US-08-833-752-4
; Sequence 4, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-752-4

Query Match 100.0%; Score 126; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 2
US-09-087-232A-17
; Sequence 17, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-087-232A-17

Query Match 100.0%; Score 126; DB 3; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

RESULT 3
US-08-833-752-6
; Sequence 6, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-752-6

Query Match 100.0%; Score 126; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 4
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 5
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillient et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA

ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 6
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELMIEBER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-861-105-14

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 7
US-08-575-967A-2
Sequence 2, Application US/08575967A
Patent No. 6265184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 126; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 8
US-09-045-583-52
Sequence 52, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: NO. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-52

Query Match 100.0%; Score 126; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114

RESULT 9
US-09-517-605-5
Sequence 5, Application US/09517605
Patent No. 6391567
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: Geijtenbeek, Ineo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
FILE OF INVENTION: 1049-1-017
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605

;; CURRENT FILING DATE: 2000-03-02
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 352
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-517-605-5

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLTGLYFIGFSS 22
Db 93 QWDFGNTMCQLTGLYFIGFSS 114

RESULT 10

US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767

GENERAL INFORMATION:

;; APPLICANT: Graham, Gerard J. et al.
;; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
;; Heptahelical Receptor Superfamily and Uses
Therefor

;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/534,185
;; FILING DATE: 24-Mar-2000
;; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 09/045,583
;; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

;; NAME: Mandragouras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 52:

;; SEQUENCE CHARACTERISTICS:
;; TYPE: amino acid
;; LENGTH: 352 amino acids
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLTGLYFIGFSS 22
Db 93 QWDFGNTMCQLTGLYFIGFSS 114

RESULT 11

US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375

GENERAL INFORMATION:

;; APPLICANT: SAMSON, MICHEL
;; APPLICANT: PARMENTIER, MARC
;; APPLICANT: VASSART, GILBERT
;; APPLICANT: LIBERT, FREDERICK
;; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Knobbe, Martens, Olson & Bear
;; STREET: 620 Newport Center Drive 16th Floor
;; CITY: Newport Beach
;; STATE: CA
;; COUNTRY: U.S.A.
;; ZIP: 92660

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/833,752
;; FILING DATE: 9-APR-1997
;; CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

;; NAME: Altman, Daniel E
;; REGISTRATION NUMBER: 34,115
;; REFERENCE/DOCKET NUMBER:
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 352 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein

US-08-833-752-5

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLTGLYFIGFSS 22
Db 93 QWDFGNTMCQLTGLYFIGFSS 114

RESULT 12

US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826

GENERAL INFORMATION:

;; APPLICANT: Li, Yi
;; APPLICANT: Ruben, Steven M.
;; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)
;; TITLE OF INVENTION: HDGMR10
;; FILE REFERENCE: 1488.1150006
;; CURRENT APPLICATION NUMBER: US/09/502,783A
;; CURRENT FILING DATE: 2001-08-23
;; PRIOR APPLICATION NUMBER: 08/466,343
;; PRIOR FILING DATE: 1995-06-06
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; TYPE: PRT
;; LENGTH: 352
;; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFFS 22

Db 93 QWDFGNTWCQLLTGLYFIIGFFS 114

RESULT 13

US-09-796-202-1
; Sequence 1, Application US/09796202

; Patent No. 6548636

; GENERAL INFORMATION:

; APPLICANT: Dragic, Tatjana

; APPLICANT: Olson, William

; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION

; FILE REFERENCE: 2048/61010/JPW/SHS

; CURRENT APPLICATION NUMBER: US/09/796,202

; CURRENT FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 352

; TYPE: PRT

; ORGANISM: human

US-09-796-202-1

Query Match 100.0%; Score 126; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.5e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFFS 22

Db 93 QWDFGNTWCQLLTGLYFIIGFFS 114

RESULT 14

US-08-466-343D-9

; Sequence 9, Application US/08466343D

; Patent No. 6025154

; GENERAL INFORMATION:

; APPLICANT: LI, Yi

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN

; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVE., NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,343D

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.1150000/BKS/KLM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 344 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-466-343D-9

Query Match 69.0%; Score 87; DB 3; Length 344;

Best Local Similarity 66.7%; Pred. No. 1.9e-05;

Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFF 21

Db 88 EWVFGNACKLFTGLYHIGYF 108

RESULT 15

US-08-461-244-3

; Sequence 3, Application US/08461244

; Patent No. 5776729

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: Yi, Li

; APPLICANT: Ruben, Steven M.

; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

; ADDRESSEE: STUART & OLSTEIN

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,244

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferraro, Gregory D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-445

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 347 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-461-244-3

Query Match 69.0%; Score 87; DB 1; Length 347;

Best Local Similarity 66.7%; Pred. No. 2e-05;

Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFF 21

Db 92 EWVFGNACKLFTGLYHIGYF 112

RESULT 16

US-08-450-393A-4

; Sequence 4, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 69.0%; Score 87; DB 1; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFF 21
DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 17
US-08-446-669-4
Sequence 4, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
REFERENCE/DOCKET NUMBER: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-4

Query Match 69.0%; Score 87; DB 3; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFF 21
DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 18
US-09-045-583-50
Sequence 50, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-50

Query Match 69.0%; Score 87; DB 3; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFF 21
DB 105 EWVFGNACKLFTGLYHIGYF 125

```

? ZIP: 92660
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
? CURRENT APPLICATION DATA: US/08/833,752
? APPLICATION NUMBER: US/08/833,752
? FILING DATE: 9-APR-1997
? CLASSIFICATION: 536
? ATTORNEY/AGENT INFORMATION:
? NAME: Altman, Daniel E
? REGISTRATION NUMBER: 34,115
? REFERENCE/DOCKET NUMBER:
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 360 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: No. 6448375e
? US-08-833-752-7

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFF 21
: ||| ||| ||| ||| |||
DB 105 EWVFGNACMKLFTGLYHIGYF 125

RESULT 21
US-09-131-827A-2
? Sequence 2, Application US/09131827A
? GENERAL INFORMATION:
? APPLICANT: Dean, Michael
? APPLICANT: O'Brien, Stephen J.
? APPLICANT: Smith, Michael
? APPLICANT: Carrington, Mary
? TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
? FILE REFERENCE: 14014.0333
? CURRENT APPLICATION NUMBER: US/09/131,827A
? CURRENT FILING DATE: 1998-08-10
? PRIOR APPLICATION NUMBER: 60/055,659
? PRIOR FILING DATE: 1997-08-14
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 2
? LENGTH: 360
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-131-827A-2

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFF 21
: ||| ||| ||| ||| |||
DB 105 EWVFGNACMKLFTGLYHIGYF 125

RESULT 22
US-09-131-827A-20
? Sequence 20, Application US/09131827A
? GENERAL INFORMATION:
? APPLICANT: Dean, Michael
? APPLICANT: O'Brien, Stephen J.
? APPLICANT: Smith, Michael

```

```
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131.827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-20

Query Match          69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCCLLTGLYFIGFF 21
Db 105 EWVFGNACMKLTGLYHIGYF 125

RESULT 23
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-00476-4

Query Match          69.0%; Score 87; DB 5; Length 360;
Best Local Similarity 66.7%; Pred. No. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCCLLTGLYFIGFF 21
Db 105 EWVFGNACMKLTGLYHIGYF 125
```

```
RESULT 24
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450.393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-2

Query Match          69.0%; Score 87; DB 1; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCCLLTGLYFIGFF 21
Db 105 EWVFGNACMKLTGLYHIGYF 125

RESULT 25
US-08-446-669-2
; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
```


SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-2

Query Match 69.0%; Score 87; DB 3; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 26
PCT-US95-00476-2
Sequence 2, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00476-2

Query Match 69.0%; Score 87; DB 5; Length 374;
Best Local Similarity 66.7%; Pred. No. 2.1e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFF 21
Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 27
US-08-307-499-30
Sequence 30, Application US/08307499
Patent No. 5651972
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,499
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-307-499-30

Query Match 65.9%; Score 83; DB 1; Length 269;
Best Local Similarity 54.5%; Pred. No. 6e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFFS 22
Db 20 QWIFGNILCKIMSVLYTVGFPS 41

RESULT 28
US-09-299-268-30
Sequence 30, Application US/09299268
Patent No. 6217882
GENERAL INFORMATION:

APPLICANT: Moyer, Richard W.
APPLICANT: Vi uela, Eladio
APPLICANT: Gibbs, E.P.J.
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
TITLE OF INVENTION: Live Vaccine Vector
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,268
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/901,127
FILING DATE:
APPLICATION NUMBER: US 07/908,241
FILING DATE: 1-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/908,630
FILING DATE: 29-JUN-1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/342,212
FILING DATE: 21-APR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-268-30

Query Match 65.9%; Score 83; DB 3; Length 269;
Best Local Similarity 54.5%; Pred. No. 6e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLLTGLTYFGTGS 22
Db 20 QWIFGNILCKIMSVLYVGGFS 41

RESULT 29
US-08-461-244-2
Sequence 2, Application US/08461244
Patent No. 5776729
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R.
APPLICANT: Yi, Li
APPLICANT: Ruben, Steven M.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN

STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-2

Query Match 65.1%; Score 82; DB 1; Length 355;
Best Local Similarity 54.5%; Pred. No. 0.00011;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLLTGLTYFGTGS 22
Db 98 QWFGTVMCKVSGFYIGFYS 119

RESULT 30
US-09-045-583-56
Sequence 56, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 56:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-56

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Query Match      65.1%; Score 82; DB 3; Length 355;
Best Local Similarity 54.5%; Pred. No. 0.00011;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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Db      98 QWDFGNTWCOLLTGLYFIFGFS 119

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Job time : 15.1429 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 18:03:03 ; Search time 29.4082 Seconds
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Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNMQLLGLXIFGFFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	126	100.0	184	9	US-09-939-226-4
4	126	100.0	184	9	US-09-938-703-4
5	126	100.0	215	9	US-09-938-719-6
6	126	100.0	215	9	US-09-939-226-6
7	126	100.0	215	9	US-09-938-703-6
8	126	100.0	332	14	US-10-085-876A-2
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89 71 56.3 355 15 US-10-452-015-2 Sequence 2, Appli
90 71 56.3 375 14 US-10-219-834-78 Sequence 78, Appl
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92 69 54.8 355 9 US-09-939-226-9 Sequence 9, Appl
93 69 54.8 355 9 US-09-938-703-9 Sequence 9, Appl
94 67 53.2 332 13 US-10-001-835-140 Sequence 140, App
95 67 53.2 355 9 US-09-931-381A-16 Sequence 16, Appl
96 67 53.2 355 9 US-09-922-895-1 Sequence 1, Appl
97 67 53.2 355 11 US-09-826-509-475 Sequence 475, App
98 67 53.2 355 13 US-10-106-623-4 Sequence 4, Appl
99 67 53.2 355 14 US-10-225-567A-64 Sequence 64, Appl
100 67 53.2 355 14 US-10-283-028-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-084-813-12
; Sequence 12, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAKINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084, 813
; PRIOR FILING DATE: 2002-02-27
; PRIOR FILING DATE: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-12

Query Match 100.0%; Score 126; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 1 QWDFGNTWCQLLTGLYFIFGFS 22

RESULT 2
US-09-938-719-4
; Sequence 4, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-938-719-4
Query Match 100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFS 114
RESULT 3
US-09-939-226-4
; Sequence 4, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-09-939-226-4

Query Match 100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFFS 22
DB 93 QWDFGNTWCQLLTGLYFIQFFS 114

RESULT 4

US-09-938-703-4
; Sequence 4, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-938-703-4

Query Match 100.0%; Score 126; DB 9; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFFS 22
DB 93 QWDFGNTWCQLLTGLYFIQFFS 114

RESULT 5

US-09-938-719-6
; Sequence 6, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-938-719-6

Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFFS 22
DB 93 QWDFGNTWCQLLTGLYFIQFFS 114

RESULT 6

US-09-939-226-6
; Sequence 6, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 09/626,939
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; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
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US-09-938-703-6

Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-09-938-703-6

Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIGFFS 114

APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6

Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIGFFS 114
```

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; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6

Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 8
US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030148294A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Bandman, Olga
; APPLICANT: Coleman, Roger; Wilde, Craig G.
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
; FILE REFERENCE: PF-0060-1 CON
; CURRENT APPLICATION NUMBER: US/10/095,876A
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 08/638,081
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

Query Match 100.0%; Score 126; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 84 QWDFGNTMCQLLTGLYFIGFFS 105

RESULT 9
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNEL10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22
Db 93 QWDFGNTMCQLLTGLYFIGFFS 114
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RESULT 12

RESULT 14
JS-09-779-880A-22

US-09-813-653-17
US-09-813-653-17 ; Sequence 17, Application US/09813653

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US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343

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/ PRIOR FILING DATE: 1995-06-06
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Artificial Sequence: Genomic
/ FEATURE:
/ OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
| | | | | | | | | | | | | | | | | | | | | |

RESULT 19
US-09-339-912A-2
/ Sequence 2, Application US/09339912A
/ Patent No. US20020099176A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Yi
/ APPLICANT: Ruben, Steven, M.
/ TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
/ FILE REFERENCE: 1488.1150003
/ CURRENT APPLICATION NUMBER: US/09/339,912A
/ CURRENT FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 09/195,662
/ PRIOR FILING DATE: 1998-11-18
/ PRIOR APPLICATION NUMBER: 08/466,343
/ PRIOR FILING DATE: 1995-06-06
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Artificial Sequence: Genomic
/ FEATURE:
/ OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
| | | | | | | | | | | | | | | | | | | | | |

RESULT 20
US-09-338-719-5
/ Sequence 5, Application US/09938719
/ Patent No. US20020106742A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
| | | | | | | | | | | | | | | | | | | | | |

RESULT 21
US-09-939-226-5
/ Sequence 5, Application US/09939226
/ Patent No. US20020110805A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
| | | | | | | | | | | | | | | | | | | | | |

RESULT 22
US-09-938-719-5
/ Sequence 5, Application US/09938719
/ Patent No. US20020106742A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
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/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/938,719
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 27-JULY-2000
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 352 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
| | | | | | | | | | | | | | | | | | | | | |

RESULT 21
US-09-939-226-5
/ Sequence 5, Application US/09939226
/ Patent No. US20020110805A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114
| | | | | | | | | | | | | | | | | | | | | |

RESULT 22
US-09-938-719-5
/ Sequence 5, Application US/09938719
/ Patent No. US20020106742A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNMCCQLLTGLYFIFGFS 22
Db 93 QWDFGNMCCQLLTGLYFIFGFS 114

RESULT 22
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SARMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNMCCQLLTGLYFIFGFS 22
Db 93 QWDFGNMCCQLLTGLYFIFGFS 114

RESULT 23
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. US20020132269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR
; TITLE OF INVENTION: HDGR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match      100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNMCCQLLTGLYFIFGFS 22
Db 93 QWDFGNMCCQLLTGLYFIFGFS 114

RESULT 24
US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; DENG, HONGKUI
; EILMEIER, WILFRIED
; LANDAU, NATHANIEL R.
; LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,221A
; FILING DATE: 11-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

Query Match          100.0%; Score 126; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFGFFS 114

RESULT 25
US-09-826-509-477
; Sequence 477, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: ARRN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 477
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-477

Query Match          100.0%; Score 126; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFGFFS 114

RESULT 26
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match          100.0%; Score 126; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFGFFS 114

RESULT 27
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:

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SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20

Query Match 100.0%; Score 126; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22
DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

RESULT 28

US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22
DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

RESULT 29

US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22
DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

RESULT 30

US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100059A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match 100.0%; Score 126; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22
DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

Search completed: March 4, 2004, 18:22:51
Job time : 29.4082 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 42.7959 Seconds

(without alignments)
118.840 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96
Sequence: 1 SQYQFWKNQTIKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_23Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	18	4	AAB88954
2	96	100.0	18	4	AAB88995
3	96	100.0	352	2	AAW27407
4	96	100.0	352	2	AAW27123
5	96	100.0	352	2	AAW07602
6	96	100.0	352	2	AAW23835
7	96	100.0	352	2	AAW88232
8	96	100.0	352	3	AAW80128
9	96	100.0	352	4	AAW07046
10	96	100.0	352	4	AAW07046
11	96	100.0	352	4	AAW07048
12	96	100.0	352	4	AAW08111
13	96	100.0	352	4	AAW04321
14	96	100.0	352	4	AAW07039
15	96	100.0	352	4	AAW07039
16	96	100.0	352	4	AAW07039
17	96	100.0	352	4	ABBS56342
18	96	100.0	352	4	ABBS3354
19	96	100.0	352	4	ABBS2948
20	96	100.0	352	5	AAU97150
21	96	100.0	352	5	AAU97150
22	96	100.0	352	5	AAU97152
23	96	100.0	352	5	AAU52829
24	96	100.0	352	5	AAU52828
25	96	100.0	352	5	ABG70597
					ABG92883

26	96	100.0	352	5	ABG92880
27	96	100.0	352	5	AAE25808
28	96	100.0	352	5	AAE25811
29	96	100.0	352	5	ABB81054
30	96	100.0	352	5	ABB808343
31	96	100.0	352	6	ABG75540
32	96	100.0	352	6	ABF58602
33	96	100.0	352	6	AAO29514
34	96	100.0	352	6	ABU61654
35	96	100.0	352	6	ABP97728
36	96	100.0	352	6	ABP81933
37	96	100.0	352	7	ADC03341
38	96	100.0	371	2	AAW23834
39	96	100.0	439	2	AAW41280
40	93	96.9	352	2	AAW27125
41	93	96.9	352	7	ADC03359
42	82	85.4	21	2	AAW50141
43	82	85.4	22	4	AAW80087
44	82	85.4	32	2	AAW43018
45	82	85.4	32	2	AAW39912
46	78	81.2	18	4	AAW88953
47	78	81.2	32	4	AAW80086
48	78	81.2	138	5	ABG32539
49	78	81.2	157	5	ABG32540
50	75	78.1	18	4	AAW88955
51	74	77.1	14	6	ABP82819
52	74	77.1	20	4	AAW83314
53	74	77.1	21	7	AAE38756
54	74	77.1	354	2	AAW54037
55	74	77.1	354	7	ADD44859
56	74	77.1	354	7	ADD44863
57	60	62.5	18	4	AAW88952
58	60	62.5	27	2	AAW46983
59	60	62.5	27	2	AAW46985
60	60	62.5	27	2	AAW46986
61	60	62.5	27	2	AAW46990
62	60	62.5	27	2	AAW46984
63	60	62.5	27	2	AAW46982
64	60	62.5	27	6	ABG75973
65	60	62.5	27	6	ABU09550
66	54	56.2	27	2	AAW46987
67	54	56.2	27	2	AAW46988
68	52	54.2	27	2	AAW46989
69	47	49.0	18	4	AAW88956
70	47	49.0	31	2	AAW40027
71	47	49.0	355	7	AAW29179
72	47	49.0	355	7	ADD45360
73	46	47.9	27	2	AAW46991
74	45	46.9	314	7	ADC01243
75	45	46.9	429	3	AAW41644
76	45	46.9	436	3	AAW41643
77	45	46.9	447	3	AAW41642
78	44	45.8	332	2	AAW26766
79	44	45.8	467	6	ABU26719
80	44	45.8	616	4	AAW88551
81	44	45.8	616	5	AAU91482
82	43	44.8	24	2	AAW23837
83	43	44.8	25	4	AAW18971
84	43	44.8	25	4	ABBS38144
85	43	44.8	25	4	AAW31572
86	43	44.8	25	4	ABBS2352
87	43	44.8	25	4	AAW71293
88	43	44.8	25	4	AAW58780
89	43	44.8	25	4	ABG53004
90	43	44.8	25	5	ABG41093
91	43	44.8	38	4	ABBS9710
92	43	44.8	38	4	AAW33287
93	43	44.8	38	4	AAW73068
94	43	44.8	38	4	AAW60428
95	43	44.8	38	4	ABG54782
96	43	44.8	38	5	ABG42912
97	43	44.8	209	5	ABP25707
98	43	44.8	232	2	AAW36078

99 43 44.8 233 4 AAM39001 Human pol
100 43 44.8 233 4 AAG89186 Human sec

ALIGNMENTS

```

RESULT 1
AAB88954
ID AAB88954 standard; peptide; 18 AA.
XX
AC AAB88954;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #47.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
PT WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
and binds to HIV gp120 under physiological conditions.
XX
PS Claim 21; Page 38; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
bind to HIV glycoprotein 120 (gp120). These are similar to the human
chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
useful in the treatment of HIV, as they prevent replication of the virus.
XX
CC The present sequence is an example of a peptide of the invention
Sequence 18 AA;
XX
SQ
Query Match 100.0%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKMFQTLKIVILG 18
DB 1 SQYQFWKMFQTLKIVILG 18

RESULT 2
AAB88995
ID AAB88995 standard; peptide; 18 AA.
XX
AC AAB88995;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #88.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
PT WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
and binds to HIV gp120 under physiological conditions.
XX
PS Example 1; Page 37; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
bind to HIV glycoprotein 120 (gp120). These are similar to the human
chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
useful in the treatment of HIV, as they prevent replication of the virus.
XX
CC The present sequence is an example of a peptide of the invention
Sequence 18 AA;
XX
SQ
Query Match 100.0%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKMFQTLKIVILG 18
DB 1 SQYQFWKMFQTLKIVILG 18

RESULT 3
AAM27407
ID AAM27407 standard; protein; 352 AA.
XX
AC AAM27407;
XX
DT 14-APR-1998 (first entry)
XX
DE Human CCR5.
XX
KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW atherosclerosis; autoimmune disorder.
XX
OS Homo sapiens.
XX
PN WO9732019-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-BE000023.
XX
PR 01-MAR-1996; 96EP-00870021.
XX
PR 06-AUG-1996; 96EP-00870102.
XX
PA (EURO-) EUROSREEN SA.
XX
PI Samson M, Parmentier M, Vassart G, Libert F;
XX
PT WPI; 1997-479829/44.
XX
DR N-PSDB; AAT90117.
XX
PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful

```

PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX
 PS Claim 4; Fig 1b-c; 94pp; English.
 XX
 CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
 CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFKNFQTLKIVILG 18
 DB 185 SQYQFKNFQTLKIVILG 202
 RESULT 4
 AAW27123
 ID AAW27123 standard; protein; 352 AA.
 XX
 AC AAW27123;
 XX
 DT 14-DEC-1997 (first entry)
 XX
 DE Human chemokine receptor 88C.
 XX
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 KW modulator; antibody; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..32
 FT /label= Extracellular_domain
 FT Domain 56..67
 FT /label= Intracellular_domain
 FT Domain 89..112
 FT /label= Extracellular_domain
 FT Domain 125..145
 FT /label= Intracellular_domain
 FT Domain 166..191
 FT /label= Extracellular_domain
 FT Domain 213..235
 FT /label= Intracellular_domain
 FT Domain 259..280
 FT /label= Extracellular_domain
 FT Domain 301..352
 FT /label= Intracellular_domain
 XX
 PN WO9722698-A2.
 XX
 PD 26-JUN-1997.
 XX
 XX 20-DEC-1996; 96WO-US020759.
 XX
 PR 20-DEC-1995; 95US-00575967.
 PR 07-JUN-1996; 96US-00661393.
 XX
 PA (ICOS-) ICOS CORP.
 XX

PI Gray PW, Schweickart VL, Raport CJ;
 XX
 DR WPI; 1997-341589/31.
 DR N-PSDB; AAT85161.
 XX
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 PT tumours, viral infections, auto-immune diseases, etc.
 XX
 XX Claim 16; Page 47-48; 65pp; English.
 XX
 CC This polypeptide sequence comprises novel human chemokine receptor 88C, a
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
 CC macrophage library. It shows 62% identity to CCR1. Chemokine receptors
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
 CC and their polypeptide fragments can be produced in transformed host
 CC cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFKNFQTLKIVILG 18
 DB 185 SQYQFKNFQTLKIVILG 202
 RESULT 5
 AAW07602
 ID AAW07602 standard; protein; 352 AA.
 XX
 AC AAW07602;
 XX
 DT 26-FEB-1997 (first entry)
 XX
 DE Human G-protein chemokine receptor HDGNR10.
 XX
 KW G-protein chemokine receptor; HDGNR10; signal transduction;
 KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9639437-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 06-JUN-1995; 95WO-US007173.
 XX
 PR 06-JUN-1995; 95WO-US007173.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Li Y, Ruben SM;
 XX
 DR WPI; 1997-043072/04.
 DR N-PSDB; AAT44042.
 XX
 PT Human G-protein chemokine receptor, HDGNR10 - useful to identify
 PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
 PT acute inflammation, rheumatoid arthritis, etc.
 XX
 PS Claim 1; Page 44-46; 61pp; English.
 XX

CC Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7
 CC -transmembrane protein involved in signal transduction. Its amino acid
 CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human
 CC monocyte library. Isolation of the cDNA allows prodn. of recombinant
 CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
 CC receptor can be used to identify agonists or antagonists of the receptor;
 CC such upds. can be used to treat conditions related to the under- and over
 CC -expression of G-protein chemokine receptors
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQFWKFNFTLKIVILG 18
 DB 185 SQQFWKFNFTLKIVILG 202

RESULT 6
 AAW23835
 ID AAW23835 standard; protein; 352 AA.

XX AC AAW23835;

XX DT 08-JUN-1998 (first entry)

XX DE Human CC chemokine receptor 5 (CCR5).

XX KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;
 XX KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Domain 29..55
 FT /label= I
 FT /note= "transmembrane domain"
 FT 104..126
 FT /label= III
 FT /note= "transmembrane domain"
 FT 109..120
 FT /note= "extracellular loop-1 (Claim 19)"
 FT 143..171
 FT /label= IV
 FT /note= "transmembrane domain"
 FT 187..210
 FT /note= "extracellular loop-2 (Claim 19)"
 FT 194..219
 FT /label= V
 FT /note= "transmembrane domain"
 FT 238..258
 FT /label= VI
 FT /note= "transmembrane domain"
 FT 261..276
 FT /note= "extracellular loop-3 (Claim 19)"
 FT 277..300
 FT /label= VII
 FT /note= "transmembrane domain"

XX PN W09745543-R2.

XX PD 04-DEC-1997.

XX PF 28-MAY-1997; 97WO-US009586.

XX PR 28-MAY-1996; 96US-0018508P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Combadriere C, Feng Y, Berger EA, Alkhatib G, Murphy PM,
 PI Broder CC, Kennedy PE;

XX WPI; 1998-032650/03.
 DR N-PSDB; AAT76920.
 XX
 CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 FT between HIV and a target cell.
 XX
 PS Claim 68; Fig 1C; 70pp; English.

XX This protein sequence comprises of a novel human macrophage-selective CC
 CC chemokine receptor that has been designated CCR5. The sequence was
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant
 CC (see W38340 of CCR5 was also identified. The susceptibility of human
 CC macrophages to HIV infection depends on cell surface expression of CD4
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
 CC protein coupled cell surface molecules. It plays an essential role in the
 CC membrane fusion step of infection by some HIV isolates. The establishment
 CC of stable, non-human cell lines and transgenic mammals having cells that
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 CC agents capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQFWKFNFTLKIVILG 18
 DB 185 SQQFWKFNFTLKIVILG 202

RESULT 7
 AAW88232
 ID AAW88232 standard; protein; 352 AA.

XX AC AAW88232;

XX DT 15-MAR-1999 (first entry)

XX DE HIV-1 co-receptor CCR5.

XX KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 XX KW gene therapy; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Domain 32..56
 FT /note= "transmembrane domain 1"
 FT 67..87
 FT /note= "transmembrane domain 2"
 FT Misc-difference 101
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 FT (Stop) in CCR5m303"
 FT Domain 103..124
 FT /note= "transmembrane domain 3"
 FT 142..167
 FT /note= "transmembrane domain 4"
 FT Domain 200..223
 FT /note= "transmembrane domain 5"
 FT Domain 236..260
 FT /note= "transmembrane domain 6"
 FT 275..301
 FT /note= "transmembrane domain 7"

XX PN W09854317-A1.

XX PD 03-DEC-1998.

XX

PF 29-MAY-1998; 98WO-EP003437.
 XX
 PR 30-MAY-1997; 97US-0048057P.
 XX
 PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 XX
 FI Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 XX WPI; 1999-059835/05.
 DR N-PSDB; AAV84126.
 XX
 PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.
 XX
 PS Disclosure; Page 34-35; 55pp; English.
 XX
 CC This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AAV84126), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SQYQFWKNFQTLKIVILG 202
 |||||
 RESULT 8
 AAY80128
 ID AAY80128 standard; protein; 352 AA.
 XX
 AC AAY80128;
 XX
 DT 19-MAY-2000 (first entry)
 XX
 DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
 XX
 KW Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumour; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.
 XX
 OS Homo sapiens.
 XX
 XX US6025154-A.
 XX
 XX 15-FEB-2000.
 XX
 PF 06-JUN-1995; 95US-00466343.
 XX
 PR 06-JUN-1995; 95US-00466343.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PI Li Y, Ruben SM;
 XX
 DR WPI; 2000-181807/16.
 DR N-PSDB; AAZ91481.
 XX
 PT Isolated nucleic acid encoding human G-protein chemokine receptor useful
 PT for diagnostic assays, scientific research and screening for compounds
 PT which bind to and activate or inhibit activation of the receptor
 PT polypeptides.
 XX
 XX Claim 1; Fig 1; 22pp; English.
 XX
 CC The present sequence represents a human G-protein chemokine receptor
 CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 CC screening for compounds which bind to and either: (1) activate the
 CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 CC healing, coagulation, and angiogenesis; treatment of solid tumours,
 CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 CC parasitic infections, psoriasis, and to stimulate growth factor activity;
 CC or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
 CC diagnostic assays for detecting diseases related to mutations in the
 CC nucleic acid sequences encoding the polypeptides and for detecting an
 CC altered level of the soluble form of the receptor polypeptides. The
 CC polynucleotides are also useful for in vitro purposes related to
 CC scientific research, synthesis of DNA and manufacture of DNA vectors
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SQYQFWKNFQTLKIVILG 202
 |||||
 RESULT 9
 AAG79089
 ID AAG79089 standard; protein; 352 AA.
 XX
 AC AAG79089;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Amino acid sequence of human CCR5 protein.
 XX
 KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX
 OS Homo sapiens.
 XX
 PN W0200164752-A2.
 XX
 XX 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006322.
 XX
 PR 02-MAR-2000; 2000US-00517605.
 XX
 PA (UTNY) UNIV NEW YORK STATE.
 PA (UTNY-) UNIV NIJMEGEN.
 XX
 PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX WPI; 2001-602565/68.
 DR
 XX An antibody for the treatment or prevention of HIV-infection comprises a

PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 PT DC-SIGN due to concomitant conformational change.

XX Disclosure; Page 118-119; 131pp; English.

CC The specification describes an antibody which is specific for an
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human CCR5 protein, which is
 CC a translocation promoting agent that interacts with CD4. This receptor
 CC functions in HIV-1 entry into cells

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
 DB 185 SQYQFWKFNQTLKIVILG 202

RESULT 10

AAE07046
 ID AAE07046 standard; protein; 352 AA.

AC AAE07046;

DT 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytosolic; immunosuppressive; neurotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..36
 FT Domain /label= Extracellular_domain
 FT 37..305
 FT Domain /label= Transmembrane_domain
 FT 37..58
 FT Domain /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT 59..67
 FT Domain /label= Intracellular_loop_1
 FT 68..88
 FT Domain /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT 89..102
 FT Domain /label= Extracellular_loop_1
 FT 103..124
 FT Domain /label= Transmembrane_domain
 FT /note= "Segment 3"
 FT 125..141
 FT Domain /label= Intracellular_loop_2
 FT 142..166
 FT Domain /label= Intracellular_loop_2

FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT 167..195
 FT Domain /label= Extracellular_loop_2
 FT 196..223
 FT Domain /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT 224..235
 FT Domain /label= Intracellular_loop_3
 FT 236..260
 FT Domain /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT 261..274
 FT Domain /label= Extracellular_loop_3
 FT 287..305
 FT Domain /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT 306..352
 FT Domain /label= Intracellular_domain

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488866/53.

XX N-PDDB; AADI3282.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.

XX Claim 102; Fig 1; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGNR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18
 DB 185 SOYQFWKFNFTLKIVILG 202

RESULT 11
 AAE07048
 ID AAE07048 standard; protein; 352 AA.

XX AAE07048;
 AC 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

OS WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181259P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

PI WPI; 2001-488966/53.

XX N-PSDB; AAD13299.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGMR10 polypeptide. Useful for preventing or treating autoimmune
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)
 HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are
 useful for treating, preventing or ameliorating a disease or disorder
 associated with inflammation, defective or aberrant chemotaxis of immune
 cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 sarcoma) or defective or aberrant T-cell antigen presenting cell
 interaction. The disease or disorder may also be an infectious disease
 (e.g. a viral infection such as an early stage HIV infection, a
 cytomegalovirus infection, or a poxvirus infection), an autoimmune
 disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 disease or disorder may be associated with aberrant CCR5 expression, lack
 of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 function. CCR5 HDGMR10 protein is used as a food additive or preservative
 to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA, a
 protein, antibodies, agonists and antagonists are also useful in the
 diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 urogenital); immune disorders (Addison's disease, allergies, autoimmune
 haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)

CC ; 'cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18

DB 185 SOYQFWKFNFTLKIVILG 202

RESULT 12

AG80111

ID AG80111 standard; protein; 352 AA.

XX AC AG80111;

XX 17-JAN-2002 (first entry)

XX Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW anti-inflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.

XX Homo sapiens.

XX WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPFP-) IPF PHARM GMBH.

XX (FORS/) FORSSMANN U.

XX Forssmann W, Adermann K, Heitland A, Spodsberg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.

XX Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;

PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-488965/53.
 DR N-PSDB; AAD13181.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX Claim 102; Fig 1; 495pp; English.
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No. 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound
 CC healing
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 DB 185 SQYQFWKNFQTLKIVILG 202
 RESULT 15
 AAE07039
 ID AAE07039 standard; protein; 352 AA.
 XX AAE07039;
 AC AAE07039;
 XX 16-OCT-2001 (first entry)
 DT
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX Homo sapiens.
 OS
 XX

PN W0200158915-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004152.
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 XX 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-488965/53.
 DR N-PSDB; AAD13198.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX Example 40; Page 486-487; 495pp; English.
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation,
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 CC a neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 CC disorders (myocardial ischaemias) and wound healing
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 DB 185 SQYQFWKNFQTLKIVILG 202
 RESULT 16
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX AAB46858;
 AC AAB46858;
 XX 16-AUG-2001 (revised)
 DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 XX Human HDGNR10 protein.
 DE
 XX HDGNR10; human; G-protein chemokine receptor; antiinflammatory;
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
 KW cytostatic; antiparasitic; antiporiatic; antirheumatic; antiarthritic;

KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
 KW hyper-eosinophilic syndrome; vulnery.

OS Homo sapiens.
 XX
 XX US2001000241-A1.
 PN
 XX
 XX 12-APR-2001.
 PD
 XX
 XX 29-NOV-2000; 2000US-00725285.
 PF
 XX
 XX 06-JUN-1995; 95US-00466343.
 PR
 XX 18-NOV-1998; 98US-00195662.
 PR
 XX 25-JUN-1999; 99US-00339912.
 PR
 XX (LIVY/) LI Y.
 PA (RUBE/) RUBEN S M.
 PA
 XX
 XX Li Y, Ruben SM;
 PI
 XX WPI; 2001-226317/23.
 DR
 XX N-PSDB; AAF26390.
 DR
 XX
 XX New human G-protein chemokine receptor polypeptides and polynucleotides,
 PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
 PT
 XX
 XX Claim 1a; Page 15; 22pp; English.

XX This invention describes a novel receptor polypeptide (I) selected from
 CC (i) a fully defined 323 amino acid sequence (II) fully disclosed in the
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
 CC products of the invention have antiinflammatory, immunomodulatory,
 CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,
 CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
 CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors, HDGRI0, (I) are useful for screening for compounds which
 CC activate or inhibit activation of (I). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 CC stimulating growth factor activity. HDGRI0 is useful for treating
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 17
 ABB56342
 ID ABB56342 standard; protein; 352 AA.

XX ABB56342;
 AC
 XX 18-FEB-2002 (first entry)
 DT
 XX

DE Non-endogenous human GPCR protein, SEQ ID NO: 477.
 XX
 XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200177172-A2.
 PN
 XX 18-OCT-2001.
 PD

XX 05-APR-2001; 2001WO-US011098.

XX 07-APR-2000; 2000US-0195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI; 2001-648759/74.

XX N-PSDB; ABI97978.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.

XX Claim 1; Page 277-278; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR
 XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 18
 AAB83354
 ID AAB83354 standard; protein; 352 AA.

XX AAB83354;

XX 09-OCT-2001 (first entry)

XX Human CCR5 protein sequence.

XX Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 KW human immunodeficiency virus; anti-inflammatory disease; human.

OS Homo sapiens.

XX EP1118858-A2.

XX 25-JUL-2001.

XX 03-JAN-2001; 2001EP-00300020.

XX 12-JAN-2000; 2000GB-00000659.

XX 12-JAN-2000; 2000GB-00000661.

XX 12-JAN-2000; 2000GB-00000663.

XX

PA (PFIZ) PFIZER LTD.
 XX (PFIZ) PFIZER INC.
 PI
 XX Dobbs S, Perros M, Rickett GA;
 XX
 DR WPI: 2001-477089/52.
 DR N-PSDB; AAF87099.
 XX
 PT Determining if an agent can modulate CCR5-gp120 interaction, comprises
 PT incubating the agent with CCR5 and gp120 and determining if the agent
 PT modulates the interaction.
 PT
 XX Claim 1; Page 110; 113pp; English.
 XX
 CC This sequence represents the human CCR5 protein sequence. The invention
 CC relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 Db 185 SQYQFWKNFQTLKIVILG 202
 |||||
 RESULT 19
 AAB82948
 ID AAB82948 standard; protein; 352 AA.
 XX
 AC AAB82948;
 XX
 DT 21-DEC-2001 (first entry)
 XX
 DE Human HIV-1 co-receptor CCR5.
 XX
 CC CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 KW infection; therapy; vaccine; anti-HIV-1.
 KW
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Binding-site 2..18
 FT /note= "binds to HIV-1 gp120"
 XX
 PN W0200164710-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006699.
 XX
 PR 29-FEB-2000; 2000US-0185667P.
 PR 19-MAY-2000; 2000US-0205839P.
 PR 07-FEB-2001; 2001US-0267231P.
 XX
 XX (PROG-) PROGENICS PHARM INC.
 PA (AARO-) ARON DIAMOND AIDS RES CENT.
 XX

PI Dragic T, Olson WC;
 XX
 DR WPI: 2001-611273/70.
 DR N-PSDB; AAH26903.
 XX
 PT Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
 PT receptor) amino terminal domain including negatively charged and two
 PT sulfated tyrosine residues is useful for treating HIV infection in
 PT humans.
 PT
 XX Claim 1; Page 30; 163pp; English.
 XX
 CC The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
 CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
 CC site that determines the specificity of the interaction between CCR5 and
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
 CC CCR5 N-terminus is required for gp120 binding and may critically modulate
 CC the susceptibility of target cells to HIV-1 infection in vivo. The
 CC invention provides claimed sulfated peptides (see AAB82947) that are
 CC based on the CCR5 N-terminal region and which are effective for
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
 CC cells from becoming infected with HIV, of treating a subject whose CD4+
 CC cells are infected with HIV, and of identifying an agent which inhibits
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
 CC out in a subject, especially a human, infected (therapeutic method), not
 CC infected with HIV (prophylactic method), or in a subject who is not
 CC infected with, but has been exposed to, HIV
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 |||||
 Db 185 SQYQFWKNFQTLKIVILG 202
 |||||
 RESULT 20
 AAU97150
 ID AAU97150 standard; protein; 352 AA.
 XX
 AC AAU97150;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 XX
 CC Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002048786-A1.
 XX
 XX 25-APR-2002.
 PD
 XX
 PF 09-FEB-2001; 2001US-00779879.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2002-434754/46.
 DR N-PSDB; ABK51853.
 XX
 PT New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX
 XX Claim 61; Fig 1; 180pp; English.
 XX
 CC The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #1
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKVILG 18
 |||||
 Db 185 SQYQFWKFNFTLKVILG 202

RESULT 21
 AAU97152
 ID AAU97152 standard; protein; 352 AA.
 XX
 AC AAU97152;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 OS Homo sapiens.
 XX
 PN US2002048786-A1.
 XX
 PD 25-APR-2002.
 XX
 XX 09-FEB-2001; 2001US-00779879.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIY/) LI Y.
 PA (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2002-434754/46.
 DR N-PSDB; ABK51870.
 XX
 PT New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX
 XX Disclosure; Page 165-166; 180pp; English.
 XX
 CC The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGNR10 #2
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKVILG 18
 |||||
 Db 185 SQYQFWKFNFTLKVILG 202

RESULT 22
 AAMS2829
 ID AAMS2829 standard; protein; 352 AA.
 XX
 AC AAMS2829;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Human CCR5 Gln 55 variant.
 XX
 KW CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification; variant.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 55 /note= "Glu replaces wild-type Leu; encoded by CTG"
 FT Misc-difference 58 /note= "Encoded by AGC"
 XX
 PN WO200171346-A2.
 XX
 PD 27-SEP-2001.
 XX
 XX 21-MAR-2001; 2001WO-US009155.
 XX
 PR 21-MAR-2000; 2000US-0190946P.

PR 21-MAR-2000; 2000US-0190996P.
 PR 21-MAR-2000; 2000US-0191299P.
 PR 20-MAR-2001; 2001US-00813448.
 PR 20-MAR-2001; 2001US-00813651.
 PR 20-MAR-2001; 2001US-00813653.
 XX (CONS-) CONSENSUS PHARM INC.
 PA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
 XX WPI; 2002-010610/01.
 DR N-PSDB; ABA02318.
 XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 PT comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.
 XX Example 3; Fig 4B; 50pp; English.
 PS The invention relates to a method for identifying a binding compound for
 CC CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention,
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided methods for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents a naturally occurring variant of human CCR5 in which
 CC there is a glutamine, rather than a leucine, at position 55
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 Db 185 SQYQFWKNFQTLKIVILG 202
 RESULT 23
 AAM52828
 ID AAM52828 standard; protein; 352 AA.
 XX AC AAM52828;
 XX DT 22-FEB-2002 (first entry)
 XX Human CC chemokine receptor 5 (CCR5).
 XX CCR5; CC chemokine receptor 5; human; HIV infection;
 XX human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 XX drug screening; identification.
 XX Homo sapiens.
 XX WC2000171346-A2.
 XX 27-SEP-2001.
 XX 21-MAR-2001; 2001WO-US009155.
 XX 21-MAR-2000; 2000US-0190946P.
 PR 21-MAR-2000; 2000US-0190996P.
 PR 21-MAR-2000; 2000US-0191299P.

PR 20-MAR-2001; 2001US-00813448.
 PR 20-MAR-2001; 2001US-00813651.
 PR 20-MAR-2001; 2001US-00813653.
 XX (CONS-) CONSENSUS PHARM INC.
 PA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
 XX WPI; 2002-010610/01.
 DR N-PSDB; ABA02317.
 XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 PT comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.
 XX Example 3; Fig 4A; 50pp; English.
 PS The invention relates to a method for identifying a binding compound for
 CC CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention,
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided methods for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents human CCR5
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 Db 185 SQYQFWKNFQTLKIVILG 202
 RESULT 24
 ABG70597
 ID ABG70597 standard; protein; 352 AA.
 XX AC ABG70597;
 XX DT 03-DEC-2002 (first entry)
 XX Human G-protein chemokine receptor, HDGNR10.
 XX Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
 XX haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
 XX chronic infection; leukaemia; T-cell mediated autoimmune disease;
 XX parasitic infection; psoriasis; growth factor activity; allergy;
 XX atherosclerosis; anaphylaxis; malignancy; inflammation; histamine;
 XX immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
 XX prostaglandin-independent fever; bone marrow failure; shock;
 XX rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
 XX immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
 XX antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
 XX antipyretic; receptor.
 XX Homo sapiens.
 OS US2002099176-A1.
 XX 25-JUL-2002.

PF 25-JUN-1999; 99US-00339912.
 XX
 PR 06-JUN-1995; 95US-00456343.
 XX
 PA (LIYY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Li Y, Ruben SM;
 XX
 DR WPI; 2002-690494/74.
 DR N-PSDB; ABS54272.
 XX
 XX Novel human G-protein chemokine receptor polypeptide useful for
 PT identifying modulators for stimulating hematopoiesis, wound healing,
 PT leukemia, for treating allergy, rheumatoid arthritis, shock and as
 PT research agents.
 XX
 PS Claim 7; Fig 1; 22pp; English.
 XX
 CC The present invention relates to the isolation of human G-protein
 CC chemokine receptor, HDGMR10 (CCR5 receptor), and the polynucleotide
 CC sequence encoding it. HDGMR10 polypeptide and polynucleotide sequences
 CC are useful for diagnosing a disease or a susceptibility to a disease
 CC related to underexpression of HDGMR10. They are useful for identifying
 CC modulators for stimulating hematopoiesis, wound healing, coagulation,
 CC angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or
 CC for stimulating growth factor activity. The sequences are also useful for
 CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,
 CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. Polynucleotide sequences encoding HDGMR10 can be
 CC used in gene therapy to treat conditions related to underexpression of
 CC HDGMR10. The present sequence represents human G-protein chemokine
 CC receptor, HDGMR10
 CC
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKQFQTLKIVILG 18
 Db 185 SQYQFWKQFQTLKIVILG 202
 RESULT 25
 ABG92883
 ID ABG92883 standard; protein; 352 AA.
 AC ABG92883;
 XX
 XX 19-NOV-2002 (first entry)
 XX Human immunoglobulin variable heavy domain #1.
 XX
 KW Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.
 XX
 OS Homo sapiens.
 XX
 XX WO200264612-A2.
 PN
 XX

PD 22-AUG-2002.
 XX
 PF 08-FEB-2002; 2002WO-US003634.
 XX
 PR 09-FEB-2001; 2001US-00779880.
 PR 09-FEB-2001; 2001WO-US004153.
 PR 12-JUN-2001; 2001US-0297257P.
 PR 08-AUG-2001; 2001US-0310458P.
 PR 12-OCT-2001; 2001US-0328447P.
 PR 21-DEC-2001; 2001US-0341725P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Roschke V, Rosen CA, Ruben SM;
 XX
 DR WPI; 2002-643455/69.
 DR N-PSDB; ABS68606.
 XX
 XX New human G-protein Chemokine Receptor gene (HDGMR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGMR10 e.g. cancer.
 XX
 PS Example 55; Fig 4; 562pp; English.
 XX
 CC The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia.
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a pneumocystis carinii infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGMR10. This is the amino acid
 CC sequence of human immunoglobulin sequence associated with the antibodies
 CC against HDGMR10
 CC
 XX Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKQFQTLKIVILG 18
 Db 185 SQYQFWKQFQTLKIVILG 202
 RESULT 26
 ABG92880
 ID ABG92880 standard; protein; 352 AA.
 XX
 XX ABG92880;
 AC
 XX 19-NOV-2002 (first entry)
 DT Human G-protein chemokine receptor (CCR5) HDGMR10 #1.
 XX
 DE Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.
 XX
 OS Homo sapiens.
 XX
 XX WO200264612-A2.
 PN
 XX

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.
 XX
 OS Homo sapiens.
 XX
 PN WO200264612-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 08-FEB-2002; 2002WO-US003634.
 XX
 PR 09-FEB-2001; 2001US-0079880.
 PR 09-FEB-2001; 2001WO-US004153.
 PR 12-JUN-2001; 2001US-0297257P.
 PR 08-AUG-2001; 2001US-0310458P.
 PR 12-OCT-2001; 2001US-0328447P.
 PR 21-DEC-2001; 2001US-0341725P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Roschke V, Rosen CA, Ruben SM;
 XX
 XX WPI; 2002-643455/69.
 DR N-PSDB; ABS68553.
 XX
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX
 PS Disclosure; Fig 1A-B; 562pp; English.
 XX
 CC The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1P8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.1B85,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence
 CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 DB 185 SQYQFWKNFQTLKIVILG 202
 RESULT 27
 AAE25808
 ID AAE25808 standard; protein; 352 AA.
 XX

AC AAE25808;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002061834-A1.
 XX
 PD 23-MAY-2002.
 XX
 PF 09-FEB-2001; 2001US-0079880.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIYI/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX
 XX WPI; 2002-499674/53.
 DR N-PSDB; AAD42409.
 XX
 XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 PT
 Claim 61; Page 163-164; 186pp; English.
 XX
 CC The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with
 CC aberrant expression of CCR5 or their ligands. They are also used for the
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGNR10 DNA
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 DB 185 SQYQFWKNFQTLKIVILG 202
 RESULT 28
 AAE25811
 ID AAE25811 standard; protein; 352 AA.
 XX
 AC AAE25811;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #2.
 XX

KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 XX US2002061834-A1.
 PN
 XX
 XX 23-MAY-2002.
 PD
 XX
 XX 09-FEB-2001; 2001US-00779880.
 PF
 XX
 XX 09-FEB-2000; 2000US-0181258P.
 PR
 XX
 XX 09-MAR-2000; 2000US-0187999P.
 PR
 XX
 XX 22-SEP-2000; 2000US-0234336P.
 XX
 XX (ROSC/) ROSEN C A.
 PA
 XX (ROSC/) ROSCHKE V.
 PA
 XX (LIYY/) LI Y.
 PA
 XX (RUBE/) RUBEN S M.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI
 XX WPI: 2002-499674/53.
 DR
 XX N-PSDB; RAD42426.
 DR
 XX
 XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 XX
 XX Disclosure; Page 170; 186pp; English.
 PS
 XX
 XX The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency (including its early stages), cytomegalovirus (CMV),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with
 CC aberrant expression of CCR5 or their ligands. They are also used for the
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGNR10 DNA
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 DB 185 SQYQFWKNFQTLKIVILG 202
 RESULT 29
 ABB81054
 ID ABB81054 standard; protein; 352 AA.
 XX
 XX ABB81054;
 AC
 XX
 XX 05-NOV-2002 (first entry)
 DT
 XX
 XX G-protein chemokine receptor, HDGNR10.
 DE
 XX
 XX 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
 KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;
 KW antirheumatic; antiarthritic; gene therapy; human; receptor.
 XX
 XX Homo sapiens.
 OS

XX US2002076745-A1.
 PN
 XX 20-JUN-2002.
 PD
 XX
 XX 18-NOV-1998; 98US-00195662.
 PF
 XX
 XX 06-JUN-1995; 95US-00456343.
 PR
 XX
 XX (LIYY/) LI Y.
 PA
 XX (RUBE/) RUBEN S M.
 XX
 XX Li Y, Ruben SM;
 PI
 XX WPI: 2002-598724/64.
 DR
 XX N-PSDB; AEN86542.
 DR
 XX
 XX New polynucleotide encoding a human G protein chemokine receptor HDGNR10,
 PT useful e.g. for treating tumors.
 PT
 XX
 XX Claim 7; Fig 1; 22pp; English.
 PS
 XX
 XX The invention relates to a novel human 7-transmembrane receptor, HDGNR10,
 CC which has been identified as a G-protein chemokine receptor. The GPCR
 CC HDGNR10 polypeptide can be expressed by standard recombinant methodology.
 CC Compounds that activate or inhibit the receptor polypeptide, optionally
 CC expressed from DNA in gene therapy vectors, are used to treat diseases
 CC that require: (a) activation of the receptor (e.g. stimulation of
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
 CC etc). The present sequence represents the human HDGNR10 receptor
 CC polypeptide
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 96; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKNFQTLKIVILG 18
 DB 185 SQYQFWKNFQTLKIVILG 202
 RESULT 30
 ABB08343
 ID ABB08343 standard; protein; 352 AA.
 XX
 XX ABB08343;
 AC
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX
 XX Human chemokine (C-C motif) receptor 5 polypeptide.
 DE
 XX
 XX Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;
 KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;
 KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;
 KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;
 KW chromosome 3p21.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 55 /label= Leu, Gln
 FT
 FT Misc-difference 162 /label= Phe, Leu
 FT
 FT Misc-difference 223 /label= Arg, Gln
 FT
 XX WO200177125-A2.
 PN
 XX

18-OCT-2001.

04-APR-2001; 2001WO-US010708.

05-APR-2000; 2000US-0194361P.

(GENA-) GENAISSANCE PHARM INC.

Choi JY, Klem SE, Koshy B;

WPI; 2002-041282/05.

N-ESDB; ABA97318, ABA97319.

New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful to diagnose and treat diseases associated with its abnormal expression or function, including human immunodeficiency virus-1 infection.

Claim 29; Fig 3; 61pp; English.

The present sequence is that of a polypeptide encoded by the human chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see ABA97318, ABA97319). The specification describes haplotyping the CCR5 gene of an individual by determining if the individual has one of the CCR5 haplotypes or haplotype pairs fully defined in the specification. The specification also describes an isolated polynucleotide comprising a nucleotide sequence which is a polymorphic variant of the reference CCR5 gene sequence and comprises an isogene defined by a haplotype described in the specification and its encoded polypeptide. The methods of the invention are useful to diagnose and develop treatment for diseases associated with abnormal expression or function of the gene. The CCR5 isogenes and the screened compounds are useful for treating human immunodeficiency virus (HIV)-1 infection and the progression to acquired immunodeficiency syndrome (AIDS). The invention has antiviral applications. The specification describes genotyping the CCR5 gene of an individual; predicting a haplotype pair for the CCR5 gene of an individual; identifying an association between a trait and a haplotype or haplotype pair of the CCR5 gene. The specification describes a composition comprising a genotyping oligonucleotide for detecting a CCR5 polymorphism; a recombinant non-human organism transformed with CCR5 polynucleotide expressing a CCR5 protein encoded by the variant sequence; an isolated antibody specific for the CCR5 polypeptide and a method for screening drugs targeting the CCR5 polypeptide

Sequence 352 AA;

Query Match 100.0%; Score 96; DB 5; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFKNFQTLKIVILG 18
|||||
DbB 185 SOYQFKNFQTLKIVILG 202

Search completed: March 4, 2004, 17:59:23
Job time : 44.7959 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 9.18367 Seconds
(without alignments)
188.535 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQQFWNFQTLKVLIG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR 78:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	352	2 A43113	chemokine (C-C) re
2	47	49.0	355	2 I49339	macrophage inflam
3	46	47.9	196	2 T22609	hypothetical prote
4	45	46.9	177	2 S34499	hypothetical prote
5	45	46.9	302	2 A75203	2-phosphoglycerate
6	45	46.9	314	2 G85575	hypothetical prote
7	45	46.9	314	2 G90724	hypothetical prote
8	45	46.9	1289	2 S67200	hypothetical prote
9	44.5	46.4	301	2 C71236	probable 2-phospho
10	44	45.8	467	2 A81263	probable integral
11	44	45.8	616	1 I54056	secretion protein
12	43	44.8	237	2 C95199	nitroreductase fam
13	43	44.8	237	2 A98066	NADPH-flavin oxido
14	43	44.8	242	2 A86719	oxidoreductase ybg
15	43	44.8	344	2 JC5942	chemokine receptor
16	43	44.8	475	2 G98183	periplasmic sorbit
17	43	44.8	3587	2 T40486	surfactin syntheta
18	42	43.8	241	2 S30843	UTR4 protein - yea
19	42	43.8	350	2 E81303	probable branched-
20	42	43.8	383	2 D90528	FAD-dependent mono
21	42	43.8	421	2 AB2915	hypothetical prote
22	42	43.8	421	2 B97689	hypothetical prote
23	42	43.8	496	2 C84678	hypothetical prote
24	41.5	43.2	159	2 H81442	hypothetical prote
25	41.5	43.2	334	2 S16296	hypothetical prote
26	41.5	43.2	334	2 A85558	ferric enterobacti
27	41.5	43.2	334	2 E90707	ferric enterobacti
28	41	42.7	46	2 I37047	NADH2 dehydrogenas
29	41	42.7	118	2 H83734	hypothetical prote

hypothetical prote
envelope-like prot
oligopeptide ABC t
hypothetical prote
NADH2 dehydrogenas
hypothetical prote
hypothetical prote
pre-mRNA splicing
probable zinc-fing
related to TOM1 pr
DNA-damage-inducib
DNA-damage-inducib
hypothetical prote
hypothetical prote
hypothetical prote
alcohol sulfotrans
hypothetical prote
hypothetical prote
chemokine (C-C) re
hypothetical prote
uncharacterized pr
transposase - frui
argininosuccinate
hypothetical prote
heat shock protein
acetate-CoA ligase
hypothetical prote
Ig heavy chain - C
hypothetical prote
hypothetical prote
hypothetical prote
competence protein
hypothetical prote
hypothetical prote
transposase all708
cell division prot
alanine racemase (
tyrosine-TRNA liga
hypothetical prote
galactosyl transfe
UDP-N-acetylmuramo
DNA modification m
DNA methyltransfer
neurotrophin-3 rec
hypothetical prote
RF1 protein - eaim
electron transfer
hypothetical prote
hypothetical prote
leukotoxin express
hypothetical prote
bo-type ubiquinol
conserved hypothet
probable type-1 se
NADH2 dehydrogenas
penicillin-binding
hypothetical prote
neurotrophin-3 rec
sensory transducti
cation transprotin
tyrosine kinase C
integral membrane
hypothetical prote
hypothetical prote
probable membrane
epimerase/dehydrat
cation efflux syst
hypothetical prote

30	41	42.7	244	2 S03215	
31	41	42.7	285	2 A84494	
32	41	42.7	303	2 I40547	
33	41	42.7	316	2 T22197	
34	41	42.7	318	2 T11833	
35	41	42.7	359	2 D83385	
36	41	42.7	456	1 E42594	
37	41	42.7	629	2 S47920	
38	41	42.7	812	2 T48016	
39	41	42.7	3839	2 T49799	
40	40.5	42.2	278	2 H91193	
41	40.5	42.2	278	2 A86041	
42	40	41.7	89	2 G97365	
43	40	41.7	163	2 G70827	
44	40	41.7	248	2 T15673	
45	40	41.7	285	1 I38548	
46	40	41.7	309	1 B64041	
47	40	41.7	324	2 T49143	
48	40	41.7	355	2 A45177	
49	40	41.7	362	2 B95611	
50	40	41.7	371	2 C97355	
51	40	41.7	376	2 S26856	
52	40	41.7	437	2 C97020	
53	40	41.7	620	2 F72395	
54	40	41.7	634	2 A83447	
55	40	41.7	672	1 A41043	
56	40	41.7	1005	2 T18537	
57	39.5	41.1	328	2 D72566	
58	39.5	41.1	467	2 T16319	
59	39	40.6	188	2 E90065	
60	39	40.6	205	2 E70199	
61	39	40.6	220	2 AFI420	
62	39	40.6	224	2 AG1795	
63	39	40.6	231	2 T26380	
64	39	40.6	241	2 AC1918	
65	39	40.6	312	2 AI2383	
66	39	40.6	335	2 T32294	
67	39	40.6	374	2 AB2488	
68	39	40.6	392	2 B69321	
69	39	40.6	404	2 F17178	
70	39	40.6	411	2 G97802	
71	39	40.6	434	2 C69397	
72	39	40.6	449	2 T44643	
73	39	40.6	452	2 JC6561	
74	39	40.6	461	2 H98255	
75	39	40.6	467	2 AC3029	
76	39	40.6	525	1 A58674	
77	39	40.6	535	2 C36811	
78	39	40.6	535	2 A37994	
79	39	40.6	548	2 C82698	
80	39	40.6	585	2 S46034	
81	39	40.6	589	2 T29895	
82	39	40.6	598	2 T14886	
83	39	40.6	623	2 T19876	
84	39	40.6	662	2 H84984	
85	39	40.6	682	2 F70421	
86	39	40.6	688	2 AI1018	
87	39	40.6	698	2 T12625	
88	39	40.6	743	2 D86888	
89	39	40.6	779	2 B81287	
90	39	40.6	803	1 S35695	
91	39	40.6	806	2 S76650	
92	39	40.6	835	2 F70363	
93	39	40.6	852	2 I51259	
94	38.5	40.1	223	2 S47654	
95	38.5	40.1	324	1 S73340	
96	38.5	40.1	541	2 T27107	
97	38.5	40.1	560	2 S64091	
98	38.5	40.1	635	2 B25558	
99	38.5	40.1	1050	2 G70396	
100	38	39.6	73	2 G96674	

ALIGNMENTS

RESULT 1
A43113
chemokine (C-C) receptor 5 - human
N/Alternate names: C-C CKR-5; CCR5
C/Species: Homo sapiens (man)
C/Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
C/Accession: A43113; S71808; A58834; A58832; G02653; A58833
R/Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A/Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A/Reference number: A43113; MUID:96241590; PMID:8639485
A/Accession: A43113
A/Molecule type: mRNA
A/Residues: 1-352 <SAMI>
A/Cross-references: GB:X91492; NID:gl262810; PIDN:CAA62796.1; PID:gl262811
M.; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Lienard, C.; Farber, C.M.; Saragosti
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.
Nature 382, 722-725, 1996
A/Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the *CXCR5* gene
A/Reference number: S71808; MUID:96345670; PMID:8751444
A/Accession: S71808
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 182-206;207-230 <SAM2>
A/Accession: A58834
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-184, 'TKSHLGAGPAACHGHLILGNPKNSASVK' <SAM3>
A/Cross-references: GB:X93939; NID:gl524062; PIDN:CAA67767.1; PID:gl524063
A/Note: This frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection
R/Combadere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A/Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor
A/Reference number: A58832; MUID:96295970; PMID:8699119
A/Accession: A58832
A/Molecule type: mRNA
A/Residues: 1-352 <COM1>
A/Cross-references: GB:U57840; NID:gl502408; PIDN:AA817071.1; PID:gl502409
A/Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R/Combadere, C.
submitted to the EMBL Data Library, May 1996
A/Reference number: H01541
A/Accession: G02653
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-89, 'L', 91-352 <COM2>
A/Cross-references: EMBL:U57840
R/Raport, C.J.; Goelling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A/Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor
A/Reference number: A58833; MUID:96291862; PMID:8663314
A/Accession: A58833
A/Molecule type: mRNA
A/Residues: 1-352 <RAP>
A/Cross-references: GB:U54994; NID:gl54994; PIDN:AA50598.1; PID:gl549946
C/Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574), and dual-tropic strains of HIV-1 bind to a complex of chemokine receptor and CXCR5
C/Genetics:
A/Gene: GDB:CMKBR5; CCR5; CXCR-5; CXCR5; ChemR13
A/Cross-references: GDB:1230510; OMIM:601373
A/Map position: 3p21-3p21
C/Function:
A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A/Note: probably acts to control granulocyte proliferation and differentiation
C/Superfamily: vertebrate rhodopsin
F/32-56/Domain: transmembrane #status predicted <TM1>
F/67-87/Domain: transmembrane #status predicted <TM2>
F/103-124/Domain: transmembrane #status predicted <TM3>

F/142-166/Domain: transmembrane #status predicted <TM4>
F/193-218/Domain: transmembrane #status predicted <TM5>
F/236-257/Domain: transmembrane #status predicted <TM6>
F/285-300/Domain: transmembrane #status predicted <TM7>
F/20-269,101-178/Disulfide bonds: #status predicted
F/268/Binding site: carbonylate (Asn) (covalent) #status predicted
F/336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F/340,343/Binding site: phosphate (Thr) (covalent) #status predicted
Query Match 100.0%; Score 96; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKNTKIVILG 18
DB 185 SOYQFWKNTKIVILG 202
RESULT 2
I49339
macrophage inflammatory protein-1 alpha receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 13-Aug-1999
C/Accession: I49339
R/Gao, J.L.; Murphy, P.M.
J. Biol. Chem. 270, 17494-17501, 1995
A/Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptors
A/Reference number: I49339; MUID:95340546; PMID:7542241
A/Accession: I49339
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-355 <RES>
A/Cross-references: EMBL:U28404; NID:g881547; PIDN:AA89153.1; PID:g881548
C/Superfamily: vertebrate rhodopsin
Query Match 49.0%; Score 47; DB 2; Length 355;
Best Local Similarity 61.5%; Pred. No. 5.6;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 6 WKNFOTLKIVILG 18
DB 195 WKNFOTLKIVILG 207
RESULT 3
T22609
hypothetical protein F54B11.8 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 04-Mar-2000
C/Accession: T22609
R/Swinburne, J.
submitted to the EMBL Data Library, March 1996
A/Reference number: Z19588
A/Accession: T22609
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-196 <WIL>
A/Cross-references: EMBL:Z70208; PIDN:CAA94143.1; GSPDB:GNC00028; CESP:F54B11.8
A/Experimental source: clone F54B11
C/Genetics:
A/Gene: CESP:F54B11.8
A/Map position: X
A/Introns: 26/1; 60/1; 94/3; 122/3
C/Superfamily: Caenorhabditis elegans hypothetical protein F54B11.8
Query Match 47.9%; Score 46; DB 2; Length 196;
Best Local Similarity 66.7%; Pred. No. 4.5;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 WKNFOTLKIVIL 17
DB 36 WKNFOTLKIVIL 47

G85575
 Nynphothetical protein Z0898 [imported] - Escherichia coli (strain O157:H7, substrain EDL958)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: G85575

A; Map position: 15R
C; Superfamily: Saccharomyces cerevisiae hypothetical protein YOR296w

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A98066
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-237 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00358.1; PID:915459219; GSPDB:GN00174
C:Genetics:
A:Gene: fip
C:Superfamily: NADPH-flavin oxidoreductase homolog
C:Keywords: oxidoreductase

Query Match 44.8%; Score 43; DB 2; Length 237;
Best Local Similarity 41.7%; Pred. No. 17;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17
||||| : : : :
DB 40 WKNFQSYVIVV 51

RESULT 14
A86719
oxidoreductase yhgA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
A:Accession: A86719
R:Rolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: A86719
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <STO>
A:Cross-references: GB:AE005176; PID:91273669; PIDN:AAK04851.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yhgA
C:Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 44.8%; Score 43; DB 2; Length 242;
Best Local Similarity 41.7%; Pred. No. 17;
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17
||||| : : : :
DB 43 WKNFQSYVIVV 54

RESULT 15
JC5942
chemokine receptor - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
A:Accession: JC5942
R:Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.
Biochem. Biophys. Res. Commun. 243, 264-268, 1998
A:Title: Cloning and characterization of a novel human chemokine receptor.
A:Reference number: JC5942; MUID:98139902; PMID:9473515
A:Accession: JC5942
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-344 <PAN>
A:Cross-references: GB:U97123; NID:92897070; PIDN:AAC35959.1; PID:92897071
C:Superfamily: vertebrate rhodopsin

Query Match 44.8%; Score 43; DB 2; Length 344;
Best Local Similarity 66.7%; Pred. No. 24;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FWKNFQTLKIVI 16
||||| : : : :
DB 195 FWKHFLLTKNNI 206

RESULT 16
G98183
periplasmic sorbitol-binding protein, smOE (AF018073) [imported] - Agrobacterium tumefac
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
A:Accession: G98183
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G98183
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK88993.1; PID:915158779; GSPDB:GN00170
C:Genetics:
A:Gene: AGR L 841
A:Map position: linear chromosome

Query Match 44.8%; Score 43; DB 2; Length 475;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 FWKNFQTLKIVILG 18
||||| : : : :
DB 34 FWEEDMTLKIVILG 47

RESULT 17
140486
surfactin synthetase component II - Bacillus subtilis
N:Alternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein s
N:Contains: acid-amino-acid ligase (EC 6.3.2.-)
C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Nov-2000
A:Accession: 140486; S60866; C69718; S46968; S35518; S2558; S34986
R:Cosmina, P.; Rodriguez, F.; de Terra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sindi
Mol. Microbiol. 8, 821-831, 1993
A:Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis
A:Reference number: 140485; MUID:93360813; PMID:8355609
A:Accession: 140486
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3587 <RES>
A:Cross-references: EMBL:X70356; NID:9396480; PIDN:CAA49817.1; PID:9396482
A:Experimental source: strain W168 derivative of JH642
R:Hansen, L.W.; Behuis, H.; Jongbloed, J.; Venema, G.; van Sinderen, D.
Mol. Microbiol. 15, 55-63, 1995
A:Title: A small gene, designated comS, located within the coding region of the fourth a
A:Reference number: S60866; MUID:95272393; PMID:7752896
A:Accession: S60866
A:Molecule type: DNA
A:Residues: 977-1104 <HAM>
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C:Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstien, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Skoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

```

QY      2 QYQFWKQFQTL 12
      :||:||||:|
Db      231 KYQVYKNFETL 241

RESULT 19
E81303
probable branched-chain amino-acid ABC transport system permease protein Cj1016c [import
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: E81303
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nautre 403, 655-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h
A;Reference number: E81250; MUID:20150912; PMID:10688204
A;Accession: E81303
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <P>R>
A;Cross-references: GB:AL139077; GB:AL111168; NID:96968444; PIDN:CA873272.1; PID:969684
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: livM; Cj1016C

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A:gene: l1vm; C:J016c

Query Match      43.8%;   Score 42;   DB 2;   Length 350;
Best Local Similarity 44.4%;   Pred. No. 36;
Matches 8;   Conservative 4;   Mismatches 6;   Indels 0;   Gaps 0;

QY      1  SQVQFKNFQTLKIVLG 18
      :|:| | | | |
Db      246  TQDFELLTQLLIIVLG 263

RESULT 20
D90528
hypotheical protein MYPU 1320 [imported] - Mycoplasma pulmonis (strain UAB CT1P)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: D90528
R:Chambaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Sanson, D.; Galissou, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
A:Reference number: A99512; PMID:21267165; PMID:11353084

```

A;Accession: D90528
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-383 <KUR>
 A;Cross-references: GB:AL445566; PID:g14089545; PIDN:CACU13305.1; GSPDB:GN00153
 A;Experimental source: strain UMB CTIP
 C;Genetics:
 A;Gene: MYP1320
 A;Genetic code: SGC3

Query Match 43.8%; Score 42; DB 2; Length 383;
 Best Local Similarity 50.0%; Pred. No. 40;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 QYQFWKNFQTLKIVIL 17
 :|||:|:|:|:
 Db 202 KFWKPKFEQKLTIL 215
 :|||:|:|:|:

RESULT 21
 AB2915
 FAB-dependent monooxygenase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AB2915
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 n; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; UID:21608550; PMID:11743193
 A;Accession: AB2915
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-421 <KUR>
 A;Cross-references: GB:AE00688; PIDN:AA43736.1; PID:g17741269; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu2755
 A;Map position: circular chromosome
 C;Superfamily: ubiH protein

Query Match 43.8%; Score 42; DB 2; Length 421;
 Best Local Similarity 46.2%; Pred. No. 44;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTLKIVIL 14
 :|||:|:|:|:
 Db 349 RYQSWRRFDTLRM 361
 :|||:|:|:|:

RESULT 22
 E97689
 hypothetical protein AGR_C_4995 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C;Species: Agrobacterium tumefaciens
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C;Accession: E97689
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappae, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A;Reference number: A97359; UID:21608551; PMID:11743194
 A;Accession: E97689
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-421 <KUR>
 A;Cross-references: GB:AE007869; PIDN:AAK88470.1; PID:g15157975; GSPDB:GN00169
 C;Genetics:
 A;Gene: AGR_C_4995
 A;Map position: circular chromosome
 C;Superfamily: ubiH protein

Query Match 43.8%; Score 42; DB 2; Length 421;
 Best Local Similarity 46.2%; Pred. No. 44;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTLKIVIL 14
 :|||:|:|:|:
 Db 349 RYQSWRRFDTLRM 361
 :|||:|:|:|:

RESULT 23
 C84678
 hypothetical protein At2g27900 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: C84678
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.
 euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; UID:20083487; PMID:10617197
 A;Accession: C84678
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-496 <STO>
 A;Cross-references: GB:AE002093; NID:g4510426; PIDN:AAD21512.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g27900
 A;Map position: 2

Query Match 43.8%; Score 42; DB 2; Length 496;
 Best Local Similarity 52.9%; Pred. No. 52;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVIL 17
 :|||:|:|:|:
 Db 100 SIHQFLKNVEDLSIFIL 116
 :|||:|:|:|:

RESULT 24
 H81442
 hypothetical protein Cj0249 [imported] - Campylobacter jejuni (strain NCTC 11169)
 C;Species: Campylobacter jejuni
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 C;Accession: H81442
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
 Nature 403, 665-668, 2000
 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
 A;Reference number: A81250; UID:20150912; PMID:10688204
 A;Accession: H81442
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-159 <PAR>
 A;Cross-references: GB:AL139074; GB:AL111168; NID:g96967505; PIDN:CAB72717.1; PID:g9696772
 A;Experimental source: serotype O2, strain NCTC 11168
 C;Genetics:
 A;Gene: Cj0249
 C;Superfamily: Campylobacter jejuni hypothetical protein Cj0249

Query Match 43.2%; Score 41.5; DB 2; Length 159;
 Best Local Similarity 40.0%; Pred. No. 20;
 Matches 8; Conservative 4; Mismatches 3; Indels 5; Gaps 1;

QY 3 YQFWKN-----FQTLKIVIL 17
 :|||:|:|:|:
 Db 33 YKFWKNAEIGRYQGTRIFL 52
 :|||:|:|:|:

RESULT 25
 SL6296
 ferric enterobactin transport protein fepD - Escherichia coli (strain K-12)

A:Gene: fopD
C:Superfamily: vitamin B12 transport protein btuC

Query Match 43.2%; Score 41.5; DB 2; Length 334;
Best Local Similarity 34.8%; Pred. No. 42;
Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;

QY 2 QYQFW-----KNFQTLKIVIL 17
Db 179 QURFWQAGSLDIRNLHLTKVLI 201

RESULT 27
E90707
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C:Accession: E90707
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99629; MUID:21156231; PMID:11258796
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90707
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA334052.1; PID:gl3360087; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECG629
C:Superfamily: vitamin B12 transport protein btuC

Query Match 43.2%; Score 41.5; DB 2; Length 334;
Best Local Similarity 34.8%; Pred. No. 42;
Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;

QY 2 QYQFW-----KNFQTLKIVIL 17
Db 179 QURFWQAGSLDIRNLHLTKVLI 201

RESULT 28
I37047
C:Species: NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - siamang mitochondrion (fragment)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 03-Jun-2002
C:Accession: I37047
R:Horai, S.; Satta, Y.; Hayasaka, K.; Kondo, R.; Inoue, T.; Ishida, T.; Hayashi, S.; Tai, J. Mol. Evol. 35, 32-43, 1992
A:Title: Man's place in Hominoidea revealed by mitochondrial DNA genealogy.
A:Reference number: I37047; MUID:92389366; PMID:1518083
A:Accession: I37047
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-46 <HOR>
A:Cross-references: GB:D38484; NID:G558513; PIDN:BA07494.1; PID:G558514
C:Genetics:
A:Gene: NDI
A:Name: mitochondrion
A:Genetic code: SGC1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 42.7%; Score 41; DB 2; Length 46;
Best Local Similarity 46.7%; Pred. No. 6;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Search completed: March 4, 2004, 18:04:01
Job time : 12.1837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 5.87755 Seconds
(without alignments)
159.465 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQYQFWKNEQLKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	352	1 CKR5 CERAE	P56493 cercopithec
2	96	100.0	352	1 CKR5 CERPY	Q9TV42 cercopithec
3	96	100.0	352	1 CKR5 CERTO	O62743 cercocobus
4	96	100.0	352	1 CKR5 GORGO	P56439 gorilla gor
5	96	100.0	352	1 CKR5 HUMAN	P51681 homo sapien
6	96	100.0	352	1 CKR5 HYLL	Q97883 hylobates 1
7	96	100.0	352	1 CKR5 HYLML	Q95NCO hylobates m
8	96	100.0	352	1 CKR5 HYSY	Q95NCS hylobates s
9	96	100.0	352	1 CKR5 PANTR	P56440 pan troglod
10	96	100.0	352	1 CKR5 PAPHA	P56441 papio hamad
11	96	100.0	352	1 CKR5 PONPY	Q97881 pongo pygma
12	96	100.0	352	1 CKR5 PYGBI	O97880 pygathrix b
13	96	100.0	352	1 CKR5 PYGNE	O97882 pygathrix n
14	96	100.0	352	1 CKR5 TRAPR	O97878 trachypithe
15	96	100.0	352	1 CKR5 TRAPH	O97879 trachypithe
16	93	96.9	352	1 CKR5 MACMU	P79436 macaca mula
17	74	77.1	354	1 CKR5 MOUSE	P51682 mus musculus
18	74	77.1	354	1 CKR5 RAT	O08556 rattus norv
19	47	49.0	355	1 CKR1 MOUSE	P51675 mus musculus
20	46	47.9	373	1 CKR2 MOUSE	P51683 mus musculus
21	45	46.9	355	1 CKR1 MACMU	P56482 macaca mula
22	45	46.9	634	1 YCK3 EUGGR	P31916 euglena gra
23	45	46.9	4523	1 DYHB HUMAN	Q96DTS homo sapien
24	44	45.8	616	1 SCRD HAEIN	P44591 haemophilus
25	43	44.8	300	1 PYRB MYCPE	Q8EUX9 mycoplasma
26	43	44.8	355	1 CKR3 CERAE	P56492 cercopithec
27	43	44.8	355	1 CKR3 MACMU	P56483 macaca mula
28	43	44.8	373	1 VIOD CHRVO	Q96JUS chromobacte
29	43	44.8	3587	1 SRF2 BACSV	Q04747 bacillus su
30	42	43.8	241	1 UTR4 YEAST	P32626 saccharomyc
31	41.5	43.2	334	1 FEPD ECOLI	P23876 escherichia
32	41	42.7	244	1 Y28K SSVU	P20213 sulfolobus
33	41	42.7	303	1 APPC BACSV	P42063 bacillus su

34	41	42.7	318	1	NULM_HYLLA	Q96126 hylobates 1
35	41	42.7	358	1	CKE3_CAVPO	Q92213 cavia porce
36	41	42.7	373	1	CKE2_RAT	O55193 rattus norv
37	41	42.7	397	1	O22B_DROME	P81910 drosophila
38	41	42.7	461	1	FCMD_HUMAN	O75072 homo sapien
39	41	42.7	629	1	PR39_YEAST	P39682 saccharomyc
40	40	41.7	284	1	SUHA_HUMAN	Q06520 homo sapien
41	40	41.7	309	1	YBCK_HAEIN	P44298 haemophilus
42	40	41.7	355	1	CKE1_HUMAN	P32246 homo sapien
43	40	41.7	371	1	Y1B0_CLOAB	Q04354 clostridium
44	40	41.7	437	1	ARLY_CLOAB	Q97K65 clostridium
45	40	41.7	501	1	AMPA_BUCBP	O89AG2 buchnera ap
46	40	41.7	634	1	HTPG_PSEAE	O913C5 pseudomonas
47	40	41.7	635	1	HTPG_PSRSM	O883Y9 pseudomonas
48	40	41.7	672	1	ACSA_METSO	P283C5 wiglesworth
49	39	40.6	78	1	Y076_WIGR	Q83C5 wiglesworth
50	39	40.6	180	1	Y16A_MYCMI	Q50239 mycoplasma
51	39	40.6	217	1	DEOC_MYCHO	P43048 mycoplasma
52	39	40.6	392	1	FTZ2_ARCFU	O29685 archaeglob
53	39	40.6	404	1	ALR_RICPR	Q92A52 rickettsia
54	39	40.6	411	1	SVY_RICCN	Q92A58 rickettsia
55	39	40.6	449	1	CPSE_STRAS	Q04664 streptococc
56	39	40.6	449	1	CPSE_STRAS	Q9AF10 streptococc
57	39	40.6	451	1	MURD_STRMU	O8DVE3 streptococc
58	39	40.6	452	1	MURD_STRPY	O8DVE3 streptococc
59	39	40.6	452	1	MURD_STRPY	O68388 streptococc
60	39	40.6	506	1	MATK_ARAAL	Q9G163 arabis alpi
61	39	40.6	535	1	V5S0_HSVSA	Q01012 herpesvirus
62	39	40.6	585	1	YB13_YEAST	P38289 saccharomyc
63	39	40.6	642	1	NOSZ_ACHCY	P94127 achromobact
64	39	40.6	662	1	CYOB_BUCAI	P57543 buchnera ap
65	39	40.6	674	1	CAN9_RAT	O35920 rattus norv
66	39	40.6	690	1	CAN9_HUMAN	O14815 homo sapien
67	39	40.6	690	1	CAN9_MOUSE	Q9D805 mus musculu
68	39	40.6	754	1	RIR1_BPT4	P32282 bacterioph
69	39	40.6	827	1	TRKC_CHICK	O91044 gallus gall
70	39	40.6	852	1	WS14_HUMAN	O9NP71 homo sapien
71	39	40.6	864	1	WS14_MOUSE	O99MZ3 mus musculu
72	38.5	40.1	324	1	MGPA_MYCPN	P75144 mycoplasma
73	38.5	40.1	560	1	GUP1_YEAST	P53154 saccharomyc
74	38	39.6	135	1	YOR6_ADEG1	P20748 avian adeno
75	38	39.6	181	1	IPYR_UREPA	O9PDH6 ureaplasma
76	38	39.6	226	1	UNG_VIBU	O8DEP7 vibrio vuln
77	38	39.6	249	1	GPM_A_ECOLI	P31217 escherichia
78	38	39.6	249	1	GPM_A_SALTY	O8ZQ62 salmonella
79	38	39.6	258	1	Y535_VIBVU	Q8DEQ1 vibrio vuln
80	38	39.6	258	1	Y659_VIBVU	Q7MMQ6 vibrio vuln
81	38	39.6	261	1	YVDC_LACLA	O9CE03 lactococcus
82	38	39.6	314	1	Y315_MYCPN	O50362 mycoplasma
83	38	39.6	389	1	O85C_DROME	O9VHQ6 drosophila
84	38	39.6	427	1	CYB6_CHILT	O59297 chlorobium
85	38	39.6	427	1	CYB6_CHITE	Q9F721 chlorobium
86	38	39.6	443	1	COBB_METJA	O58816 methanococc
87	38	39.6	459	1	Y226_MYGE	P47468 mycoplasma
88	38	39.6	502	1	MATK_SINAL	P09364 sinapis alb
89	38	39.6	503	1	Y226_MYCPN	P75462 mycoplasma
90	38	39.6	526	1	ALG8_HUMAN	O9BVK2 homo sapien
91	38	39.6	581	1	FUR4_SCHPO	Q10279 schizosacch
92	38	39.6	598	1	Y036_HUMAN	Q15051 homo sapien
93	38	39.6	879	1	MANB_BOVIN	Q93444 bos taurus
94	38	39.6	879	1	MANB_CAPI	O95327 capra hircu
95	38	39.6	879	1	MANB_HUMAN	O00462 homo sapien
96	38	39.6	940	1	SVI_BUCAI	P57249 buchnera ap
97	38	39.6	965	1	PT03_YEAST	P32522 saccharomyc
98	38	39.6	1505	1	CUT2_HUMAN	O14529 homo sapien
99	37.5	39.1	304	1	HEMZ_THEVO	Q978U9 thermoplasm
100	37.5	39.1	308	1	HEMZ_THEAC	Q9H1B8 thermoplasm

ALIGNMENTS

RESULT 1

CCR5 CERAE
 ID CCR5 CERAE STANDARD; PRT; 352 AA.
 AC P56493;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKR5.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Kidney;
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhlmann S.B., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses."; J. Virol. 71:8642-8656(1997).
 RL J. Virol. 71:8642-8656(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
 RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
 RT gene."; Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; U83324; AAC51795.1; -;
 CC EMBL; U83325; AAC51796.1; -;
 CC EMBL; AB015944; BAA31328.1; -;
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
 CC PROSITE; PS50262; G PROTEIN RECP FL 2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 CC Polymorphism.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

FT VARIANT 14 14 N -> Y.
 FT VARIANT 352 352 F -> L.
 SQ SEQUENCE 352 AA; 40561 MW; 79528690C72EC29A CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQFWKFNQTLKIVILG 18
 DB 185 SQYQFWKFNQTLKIVILG 202
 RESULT 2
 ID CCR5 CERPY STANDARD; PRT; 352 AA.
 AC Q9TV42;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKR5.
 OS Cercopithecus pygerythrus (Vervet monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=60710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=100;
 RX MEDLINE=99335215; PubMed=10408730;
 RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
 RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomgaard A.;
 RT "Mutations in CCR5-coding sequences are not associated with HIV
 RT carrier status in African nonhuman primates."; AIDS Res. Hum. Retroviruses 15:931-939(1999).
 RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF035222; AAD44015.1; -;
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
 CC PROSITE; PS50262; G PROTEIN RECP FL 2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SQYQFWKFNQTLKIVILG 18
 Db 185 SQYQFWKFNQTLKIVILG 202
 RESULT 3
 ID_CKRS_CERTO STANDARD; PRT; 352 AA.
 AC O62743; O62744; O62745; O62746;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKR5.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecidae;
 OC NCBI_TaxID=9531;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=Isolate 079, 085, 087, and 089;
 RX MEDLINE=98321155; PubMed=9656999;
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
 RT "Primary HIV isolates use the CCR5 coreceptor from sooty mangabeys
 RT naturally infected in west Africa: a comparison of coreceptor usage
 RT of primary HIV-1, HIV-2, and SIVmac.";
 RL Virology 246:113-124 (1998).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC EMBL; AF051902; AAC39830.1; -
 CC EMBL; AF051903; AAC39831.1; -
 CC EMBL; AF051904; AAC39832.1; -
 CC EMBL; AF051905; AAC39833.1; -
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 250 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT VARIANT 15 15 SULFATION (BY SIMILARITY).
 FT VARIANT 2 2 D -> E (IN ISOLATE 087).
 FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
 FT VARIANT 25 25 V -> G (IN ISOLATE 079).
 FT VARIANT 100 100 M -> K (IN ISOLATE 079).
 FT VARIANT 107 107 L -> V (IN ISOLATE 089).
 FT VARIANT 134 134 V -> G (IN ISOLATE 079).
 FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
 FT VARIANT 340 340 T -> I (IN ISOLATE 079).
 SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47B49CA CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SQYQFWKFNQTLKIVILG 18
 Db 185 SQYQFWKFNQTLKIVILG 202
 RESULT 4
 ID_CKRS_GORGO STANDARD; PRT; 352 AA.
 AC P56439;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKR5.
 OS Gorilla gorilla gorilla (Lowland gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
 OC NCBI_TaxID=9595;
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=97269687; PubMed=9108095;
 RA Klinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AF005659; AAB62553.1; -
 CC InterPro: IPR000276; GPCR_Rhodpsn.
 CC Pfam: PF00001; 7tm1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; P500237; G PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; P50262; G PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40515 MW; DO66FCB9FE5EAC84 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWNQTGLKIVILG 18
 DB 185 SQYQFWNQTGLKIVILG 202

RESULT 5
 CCR5 HUMAN
 ID CCR5_HUMAN STANDARD; PRT; 352 AA.
 AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;
 AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
 AC O14708; O15538; Q9UPA4;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
 DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
 GN CCR5 OR CMKBR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96241590; PubMed=8639485;
 RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
 RT "Molecular cloning and functional expression of a novel human
 CC chemokine receptor gene."
 RL Biochemistry 35:3362-3367(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96291862; PubMed=8663314;
 RA Raport C.J., Gosling J., Schwechardt V.L., Gray P.W., Charo I.F.;
 RT "Molecular cloning and functional characterization of a novel human
 CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."
 RL J. Biol. Chem. 271:17161-17166(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96295970; PubMed=8699119;
 RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
 RT "Cloning and functional expression of CC CKR5, a human monocyte CC
 chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
 RANTES."
 RL J. Leukoc. Biol. 60:147-152(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Ghoj L., Ia Bastide M., Kaplan N., Greco T., Touchman J.,
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
 RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses."
 RL J. Virol. 71:8642-8656(1997).
 RN [6]
 RP SEQUENCE FROM N.A. AND POLYMORPHISMS.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049523; PubMed=9388201;
 RA Mummidi S., Ahuja S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 RT with 5'-end heterogeneity, dual promoter usage, and evidence for
 RT polymorphisms within the regulatory regions and noncoding exons."
 RL J. Biol. Chem. 272:30662-30671(1997).
 RN [8]
 RP SEQUENCE FROM N.A. AND VARIANT ARG-178.
 RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
 RA Debre P.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260017; PubMed=8649511;
 RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,
 RA di Marzio P., Broder C., Sauton R.E., Hill C.M., Davis C.B.,
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 RT HIV-1."
 RL Nature 381:661-666(1996).
 RN [11]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260018; PubMed=8649512;
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 RT CC-CKR-5."
 RL Nature 381:667-673(1996).
 RN [12]
 RP SULFATION.
 RX MEDLINE=99189752; PubMed=10089882;
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Gayabab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 RT entry."
 RL Cell 96:667-676(1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and rantes and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or

differentiation. Acts as co-receptor with CD4 for primary non-syngium-inducing strains (NSI) (macrophage-tropic) of HIV-1 virus. It promotes Env-mediated fusion of the virus.

-|- SUBCELLULAR LOCATION: Integral membrane protein.

-|- TISSUE SPECIFICITY: Found in promyelocytic cells.

-|- PTM: Sulfation contributes to the efficiency of HIV-1 entry.

-|- PTM: Modified by O-linked glycosylation, but not by N-linked glycosylation.

-|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; X91492; CAA62796.1; -
 DR EMBL; U54994; AAC50598.1; -
 DR EMBL; U57840; AAB17071.1; -
 DR EMBL; U95626; AAB57793.1; -
 DR EMBL; U83326; AAC51797.1; -
 DR EMBL; AF011500; AAB65700.1; -
 DR EMBL; AF011501; AAB65701.1; -
 DR EMBL; AF011502; AAB65702.1; -
 DR EMBL; AF011503; AAB65703.1; -
 DR EMBL; AF011504; AAB65704.1; -
 DR EMBL; AF011505; AAB65705.1; -
 DR EMBL; AF011506; AAB65706.1; -
 DR EMBL; AF011507; AAB65707.1; -
 DR EMBL; AF011508; AAB65708.1; -
 DR EMBL; AF011509; AAB65709.1; -
 DR EMBL; AF011510; AAB65710.1; -
 DR EMBL; AF011511; AAB65711.1; -
 DR EMBL; AF011512; AAB65712.1; -
 DR EMBL; AF011513; AAB65713.1; -
 DR EMBL; AF011514; AAB65714.1; -
 DR EMBL; AF011515; AAB65715.1; -
 DR EMBL; AF011516; AAB65716.1; -
 DR EMBL; AF011517; AAB65717.1; -
 DR EMBL; AF011518; AAB65718.1; -
 DR EMBL; AF011519; AAB65719.1; -
 DR EMBL; AF011520; AAB65720.1; -
 DR EMBL; AF011521; AAB65721.1; -
 DR EMBL; AF011522; AAB65722.1; -
 DR EMBL; AF011523; AAB65723.1; -
 DR EMBL; AF011524; AAB65724.1; -
 DR EMBL; AF011525; AAB65725.1; -
 DR EMBL; AF011526; AAB65726.1; -
 DR EMBL; AF011527; AAB65727.1; -
 DR EMBL; AF011528; AAB65728.1; -
 DR EMBL; AF011529; AAB65729.1; -
 DR EMBL; AF011530; AAB65730.1; -
 DR EMBL; AF011531; AAB65731.1; -
 DR EMBL; AF011532; AAB65732.1; -
 DR EMBL; AF011533; AAB65733.1; -
 DR EMBL; AF011534; AAB65734.1; -
 DR EMBL; AF011535; AAB65735.1; -
 DR EMBL; AF011536; AAB65736.1; -
 DR EMBL; AF011537; AAB65737.1; -
 DR EMBL; AF031237; AAB94735.1; -
 DR EMBL; AF052539; AAD18131.1; -
 DR EMBL; AY221093; AAO65971.1; -
 DR EMBL; HGNC:1606; CCR5.
 MIM; 601373; -
 DR GO; GO:0005768; C:cytosol; TAS.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; TAS.
 DR GO; GO:0015026; F:coreceptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0006968; P:cellular defense response; TAS.
 DR GO; GO:0006935; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0007125; P:invasive growth; TAS.
 DR GO; GO:0007203; P:phosphatidylinositol-4,5-bisphosphate hydro. . .; TAS.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.
 DR PROSITE; PS0262; G PROTEIN RECP Fl 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 KW Polymorphism.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).

Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWNFKTLKIVILG 18
 |||||
 Db 185 SQYQFWNFKTLKIVILG 202

RESULT 6
 CCR5 HYLL
 ID CCR5 HYLL STANDARD; PRT; 352 AA.
 AC 097883;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Hylobates leucogynus (White-cheeked gibbon).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=61853;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -|- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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EMBL; AF075451; AAD19863.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.
 DR PROSITE; PS0262; G PROTEIN RECP Fl 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 5 (POTENTIAL).
 FT TRANSMEM 199 218 6 (POTENTIAL).
 FT DOMAIN 219 235 7 (POTENTIAL).
 FT TRANSMEM 236 260 8 (POTENTIAL).
 FT DOMAIN 261 277 9 (POTENTIAL).
 FT TRANSMEM 278 301 10 (POTENTIAL).
 FT DOMAIN 302 352 11 (POTENTIAL).
 FT DISULFID 101 178 12 (POTENTIAL).
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40445 MW; 4FB84F344CEB7C91 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.6e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
 |||||
 DB 185 SQYQFWKFNQTLKIVILG 202

RESULT 7
 CKR5_HYLM
 ID CKR5_HYLM STANDARD; PRT; 352 AA.
 AC Q95NC5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
 GN CC5 OR CMKERS.
 OS Hylobates moloch (Silvery gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=81572;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 or send an email to license@isb-sib.ch).

EMBL; AF177899; AAK43382.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124

FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 5 (POTENTIAL).
 FT TRANSMEM 199 218 6 (POTENTIAL).
 FT DOMAIN 219 235 7 (POTENTIAL).
 FT TRANSMEM 236 260 8 (POTENTIAL).
 FT DOMAIN 261 277 9 (POTENTIAL).
 FT TRANSMEM 278 301 10 (POTENTIAL).
 FT DOMAIN 302 352 11 (POTENTIAL).
 FT DISULFID 101 178 12 (POTENTIAL).
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.6e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
 |||||
 DB 185 SQYQFWKFNQTLKIVILG 202

RESULT 8
 CKR5_HYLSY
 ID CKR5_HYLSY STANDARD; PRT; 352 AA.
 AC Q95NC5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
 GN CC5 OR CMKERS.
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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EMBL; AF177884; AAK43367.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124

"Sequence comparison of the CCR5 gene in primates and primate phylogeny";

RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

RL MIP-1 FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role

CC in the control of granulocytic lineage proliferation or

CC differentiation.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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DR EMBL; AF005663; AAB62557.1; -;

DR EMBL; U94329; AAB58446.1; -;

DR EMBL; AF011542; AAB65742.1; -;

DR EMBL; U97666; AAC51670.1; -;

DR EMBL; AF011540; AAB65740.1; -;

DR EMBL; U89797; AAC33717.1; -;

DR EMBL; AF177894; AAK43377.1; -;

DR InterPro; IPR000276; GPCR_Rhodopn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PRQ0237; GPCRHDOPSN

DR PROSITE; PS02037; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

KW EXTRACELLULAR (POTENTIAL).

FT DOMAIN 1 30

FT TRANSMEM 31 58

FT CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 59 68

FT CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 90 102

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 125 141

FT CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 167 198

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 199 218

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 219 235

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 236 260

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 261 277

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 301

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 302 352

FT BY SIMILARITY.

FT DISULFID 101 178

FT MOD_RES 3 3

FT SULFATION (BY SIMILARITY).

FT MOD_RES 10 10

FT SULFATION (BY SIMILARITY).

FT MOD_RES 14 14

FT SULFATION (BY SIMILARITY).

FT MOD_RES 15 15

FT SULFATION (BY SIMILARITY).

FT CARBOHYD 268 268

FT N-LINKED GLCNAC... (POTENTIAL).

FT CONFLICT 123 123

T -> S (IN REF. 1).

SS SEQUENCE 352 AA; 40539 MW; 4A33E69B80FE34C CRC64;

GN CCR5 OR CMKRS.
 OS Papio hamadryas (Hamadryas baboon), and
 RA Papio anubis (Olive baboon)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=9557, 9555;
 RN [1]
 RC SPECIES FROM N.A.
 RC SPECIES=P.hamadryas;
 RX MEDLINE=9726867; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC SPECIES=P.hamadryas;
 RC SPECIES=P.hamadryas;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
 RT "Species-specific changes in the CCR5 gene from African and Asian
 RT nonhuman primates";
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC SPECIES=P. anubis;
 RA Benton P.A., Tinsley D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC
 DR EMBL; AF005658; AAC62552.1; -;
 DR EMBL; AF105287; AAD20556.1; -;
 DR EMBL; AF105288; AAD20557.1; -;
 DR EMBL; AF105289; AAD20558.1; -;
 DR EMBL; AF105290; AAD20559.1; -;
 DR EMBL; AF023452; AAC63830.1; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1 1; 1.
 DR PROSITE; PS0262; G PROTEIN RECP F1 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 302 7 (POTENTIAL).
 FT DOMAIN 303 352 CYTOPLASMIC (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 FT CARBOHYD 268 268 N-LINKED (GLCNAc. .) (POTENTIAL).
 SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FEB82 CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Fred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SQYQWKNFQTLKIVIG 18
 DB 185 SQYQWKNFQTLKIVIG 202
 RESULT 11
 CCR5 PONY STANDARD; PRT; 352 AA.
 AC 097881;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKRS.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC
 DR EMBL; AF075446; AAD19858.1; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1 1; 1.
 DR PROSITE; PS0262; G PROTEIN RECP F1 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
 |||||
 Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 12
 CKR5 PYGBI
 ID CKR5 PYGBI STANDARD; PRT; 352 AA.
 AC O97880;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 OC NCBI_TaxID=61621;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AF075445; AAD19857.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PS00237; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
 |||||
 Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 13
 CKR5 PYGNE
 ID CKR5 PYGNE STANDARD; PRT; 352 AA.
 AC O97882;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Pygathrix nemaeus (Dove langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 OC NCBI_TaxID=54133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AF075448; AAD19860.1; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PS00237; GPCRHOOPS.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).

FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E61 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 14

CKR5_TRAFR
 ID CKR5_TRAFR STANDARD; PRT; 352 AA.
 AC O97878;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CCR5.
 OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Trachypithecus.
 OC NCBI_TaxID=54180;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF075442; AAD19854.1;
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHOOPS.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
 |||||
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 15

CKR5_TRAFR
 ID CKR5_TRAFR STANDARD; PRT; 352 AA.
 AC O97879;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CCR5.
 OS Trachypithecus phayrei (Phayre's leaf monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Trachypithecus.
 OC NCBI_TaxID=61618;
 OX [1]
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 MIP-1-beta and RANTES and subsequently transduces a signal by
 increasing the intracellular calcium ions level. May play a role
 in the control of granulocytic lineage proliferation or
 differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL: AF075443; AAD19855.1;
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHOOPS.
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 267 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40509 MW; 4366F148D9A5398F CRC64;
 Query Match 100.0%; Score 96; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SOYQFWKFNQTLKIVILG 18
 Db 185 SOYQFWKFNQTLKIVILG 202
 RESULT 16
 CCR5_MACMU
 ID CCR5_MACMU STANDARD; PRT; 352 AA.
 AC 279436; 002746;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKR5.
 OS Macaca mulatta (Rhesus macaque),
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544, 9541, 9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta;
 RX MEDLINE=97184592; PubMed=9032394;
 RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
 RA Newman W., Gerard N., Gerard C., Sodroski J.;
 RT "Utilization of C-C chemokine receptor 5 by the envelope
 RT glycoproteins of a pathogenic simian immunodeficiency virus,
 RT SIVmac239.";
 RL J. Virol. 71:2522-2527(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta; STRAIN=Indian macaque;
 RX MEDLINE=97213934; PubMed=9060623;
 RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
 RA "Genetically divergent strains of simian immunodeficiency virus use
 RT CCR5 as a coreceptor for entry.";
 RL J. Virol. 71:2705-2714(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta;
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors.";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Sansom M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC EMBL; U77672; AAC51109.1; -;
 CC EMBL; U73739; AAC51158.1; -;
 CC EMBL; U96762; AAC34132.1; -;
 CC EMBL; AF005660; AAB62554.1; -;
 CC EMBL; AF005661; AAB62555.1; -;
 CC EMBL; AF005662; AAB62556.1; -;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF0001; 7cm.1; 1.
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 241 241 M -> I (IN REF. 3).
 FT CONFLICT 292 292 I -> M (IN REF. 3).
 SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;
 Query Match 96.9%; Score 93; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SOYQFWKFNQTLKIVILG 18
 Db 185 SOYQFWKFNQTLKIVILG 202
 RESULT 17
 CCR5_MOUSE
 ID CCR5_MOUSE STANDARD; PRT; 354 AA.
 AC PS1682; O35313; O35891; P97308; P97405; Q61867;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (MIP-1
 DE alpha receptor).
 GN CCR5 OR CMKR5.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Spleen;
 RX MEDLINE=96205938; PubMed=8631787;
 RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
 RA Charo I.P.;
 RT "Molecular cloning and functional expression of murine JE (monocyte
 RT chemottractant protein 1) and murine macrophage inflammatory protein
 RT 1 alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.";
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=96278910; PubMed=8662890;
 RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "Cloning and characterization of a novel murine macrophage
 RT inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 271:14445-14451(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola;
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=97404635; PubMed=9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Zhang T.Y., Cen Y.H.,
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 RT immunodeficiency virus type 1.";
 RL J. Virol. 71:6305-6314(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC Guo B., Kuno K., Harada A., Matsushima K.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
 CC but not in nonhematopoietic cell lines.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; U47036; AAC52454.1; -
 CC EMBL; X94151; CAB3867.1; -
 CC EMBL; U68565; AAB37273.1; -
 CC EMBL; U83327; AAC53386.1; -
 CC EMBL; AF022990; AAC53389.1; -
 CC EMBL; AF019772; AAB71183.1; -
 CC EMBL; D83648; BAA12024.1; -
 CC MGJ:107182; CCR5.

DR GO; GO:0016493; E-C-C chemokine receptor activity; IDA.
 DR GO; GO:0006952; P:defense response; IMP.
 DR InterPro; IPR000276; GPCR Rhodpsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN RECF1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECF1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 FT DOMAIN 1 32
 FT TRANSMEM 33 60
 FT DOMAIN 61 70
 FT TRANSMEM 71 91
 FT DOMAIN 92 104
 FT TRANSMEM 105 126
 FT DOMAIN 127 143
 FT TRANSMEM 144 168
 FT DOMAIN 169 200
 FT TRANSMEM 201 220
 FT DOMAIN 221 237
 FT TRANSMEM 238 262
 FT DOMAIN 263 279
 FT TRANSMEM 280 303
 FT DOMAIN 304 354
 FT DISULFID 103 180
 FT CARBOHYD 270 270
 FT VARIANT 11 11
 FT VARIANT 62 62
 FT VARIANT 66 66
 FT VARIANT 97 97
 FT VARIANT 109 109
 FT VARIANT 156 156
 FT VARIANT 160 160
 FT VARIANT 185 185
 FT VARIANT 213 213
 FT VARIANT 318 318
 FT VARIANT 337 337
 FT CONFLICT 3 3
 FT CONFLICT 80 80
 FT CONFLICT 145 145
 FT CONFLICT 190 190
 FT CONFLICT 208 208
 SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;
 Query Match 77.1%; Score 74; DB 1; Length 354;
 Best Local Similarity 76.5%; Pred. No. 0.002; 1; Indels 0; Gaps 0;
 Matches 13; Conservative 3; Mismatches 1;
 QY 1 SQYQFWKVFQTLKIVIL 17
 DB 187 TOYHFWKSFQTLKIVIL 203
 RESULT 18
 CCR5_RAT
 ID CCR5_RAT STANDARD; PRT; 354 AA.
 AC O08556;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (MIP-1
 DE alpha receptor).
 GN CCR5 OR CCR5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=98334064; PubMed=9670989;
 RA Spleiss O., Gourma N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
 RA Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and


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DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 55 55 M -> V (IN REF. 2 AND 3).
FT CONFLICT 149 149 L -> F (IN REF. 3).
FT CONFLICT 278 278 H -> Q (IN REF. 3).
SQ SEQUENCE 355 AA; 40901 MW; FCB9FF70B6F38B1 CRC64;

Query Match 49.8%; Score 47; DB 1; Length 355;
Best Local Similarity 61.5%; Pred. No. 3.9;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
DB 195 WKRFQALINLLG 207

RESULT 20
CKR2_MOUSE
ID CKR2_MOUSE STANDARD; PRT; 373 AA.
AC P51683; Q61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2) (CCR2)
DE (JE/FIC receptor) (MCP-1 receptor).
GN CCR2 OR CMKR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787;
RA Borling L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.P.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT 1alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9."
RL J. Biol. Chem. 271:7551-7558 (1996).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=96216064; PubMed=8662823;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
RT the C-C chemokines JE and FIC."
RL J. Biol. Chem. 271:11603-11606 (1996).
RN [3]
SEQUENCE FROM N.A.
RP MEDLINE=97026720; PubMed=8872898;
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA Post T.W., Gerard C., Dorff M.E.;

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RT *Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
RT transcriptase-polymerase chain reaction does not detect mRNA for the
RT KC or new MCP-1 receptor."
RL J. Neurosci. Res. 45:382-391 (1996).
CC -I- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U47035; AAC52453.1; -
CC EMBL; U51717; AAC52557.1; -
CC EMBL; U56619; AAC52784.1; -
CC GCD; MG1:106185; Ccr2.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0019955; F:cytokine binding; IPI.
CC GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
CC GO; GO:0030097; P:hemosiderin; IMP.
CC GO; GO:0006959; P:humoral immune response; IMP.
CC GO; GO:0006954; P:inflammatory response; IMP.
CC GO; GO:0030334; P:regulation of cell migration; IMP.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 83 1 (POTENTIAL).
FT DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 94 114 2 (POTENTIAL).
FT DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 128 149 3 (POTENTIAL).
FT DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 239 5 (POTENTIAL).
FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 281 6 (POTENTIAL).
FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 299 322 7 (POTENTIAL).
FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203 BY SIMILARITY.
FT CONFLICT 39 39 Y -> H (IN REF. 1).
FT CONFLICT 184 184 A -> G (IN REF. 1).
FT CONFLICT 264 264 V -> G (IN REF. 1).
SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 47.9%; Score 46; DB 1; Length 373;
Best Local Similarity 64.3%; Pred. No. 5.8;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 QFWKRFQTLKIVIL 17
DB 209 QLWKNFQTLKIVIL 222

RESULT 21
CKR1_MOUSE
ID CKR1_MOUSE STANDARD; PRT; 355 AA.
AC P56482;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)

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Hypothetical 78.0 kDa protein in F5BC intron 2 (ORF635).

DE OS Euglena gracilis.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX NCBI_TaxID=3039;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z / UTEX 753;
RA MEDLINE=93347989; PubMed=8346031;
RX Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,
RY Orsat B., Spielmann A., Stutz E.;
RT "Complete sequence of Euglena gracilis chloroplast DNA."
RL Nucleic Acids Res. 21:3537-3544 (1993).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstat-
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z11874; -; NOT ANNOTATED_CDS.
DR EMBL: X70810; CAA50080.1; -.
DR PIR: S34499; S34499.
DR PIR: S34500; S34500.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 634 AA; 78049 MW; D966B8864519E334 CRC64;
Query Match 46.9%; Score 45; DB 1; Length 634;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 2; Indels 4; Gaps

QY 4 QFW----KNFQTILKIVIL 17
DB :|||:|||||:
60 KPWDSQIKNFMTLKIKL 77

RESULT 23

ID DVHB HUMAN STANDARD; PRT; 4523 AA.
AC Q96DT5; Q9UJ22;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ciliary dynein heavy chain 11 (Axonemal beta dynein heavy chain 11).
GN DNAB11
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.; VARIANT PCD GLN-3004, AND VARIANTS LEU-34;
RC ARG-639; CYS-654; ALA-1023; THR-1038; GLY-1640; ASN-2641; THR-3474;
RX VAL-3715; PRO-3765 AND ILE-4177.
RY TISSUE=Nasal epithelium, and Testis;
MD MEDLINE=22155903; PubMed=12142464;
RA Bartoloni L., Blouin J.L., Pan Y., Gehrig C., Maiti A.K., Scamuffa N.,
RA Rossier C., Jorissen M., Armentot M., Meeks M., Mitchison H.M.,
RA Chung E.M., Delozier-Blanchet C.D., Craigen W.J., Antonarakis S.E.;
RT "Mutations in the DNAB11 (axonemal heavy chain dynein type 11) gene
RT cause one form of situs inversus totalis and most likely primary
RT ciliary dyskinesia."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10282-10286 (2002).
CC [2]
CC SEQUENCE OF 1904-2004 FROM N.A.
DR TISSUE=Nasal polyps;
DR Maiti A.K., Mattei M.-G., Jorissen M., Volz A., Ziegler A.,
DR Bouvagnet P.;
RT "Chromosomal localization of human dynein heavy chain genes."
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Force generating protein of respiratory cilia. Produces
CC force towards the minus ends of microtubules. Dynein has ATPase

activity; the force-producing power stroke is thought to occur on release of ADP.

-!- SUBUNIT: Consists of at least two heavy chains and a number of intermediate and light chains.

-!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem (which binds cargo and interacts with other dynein components), and the head or motor domain. The motor contains six tandemly-linked AAA domains in the head, which form a ring. A stalk-like structure (formed by two of the coiled coil domains) protrudes between AAA 4 and AAA 5 and terminates in a microtubule-binding site. A seventh domain may also contribute to this ring; it is not clear whether the N-terminus or the C-terminus forms this extra domain. There are four well-conserved and two non-conserved ATPase sites, one per AAA domain. Probably only one of these (within AAA 1) actually hydrolyzes ATP, the others may serve a regulatory function.

-!- DISEASE: Defects in DNAH11 are a cause of primary ciliary dyskinesia (PCD) [MIM:242650]; also known as immotile cilia syndrome 1 (ICS1). The phenotype of this autosomal recessive disease is characterized by axonemal abnormalities of respiratory cilia and sperm tails leading to bronchiectasis and sinusitis, which are sometimes associated with situs inversus (Kartagener syndrome) and male sterility.

-!- SIMILARITY: Belongs to the dynein heavy chain family.

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EMBL; AJ320497; CAC60121.1; -
EMBL; AJ132087; CAA10560.1; -
Genew; HGNC:2942; DNAH11.
MIM; 603339; -
MIM; 242650; -
GO; GO:0003858; C:axonemal dynein complex; NAS.
GO; GO:0003775; F:axonemal motor activity; NAS.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR004273; Dynein heavy.
Pfam; PF03028; Dynein heavy; 1.
SMART; SM00382; AAA; 4.
Motor protein; Dynein; Microtubule; ATP-binding; Repeat; Coiled coil;
Polymorphism; Disease mutation.
DOMAIN 1 1861
STEM (BY SIMILARITY).
AAA 1 (BY SIMILARITY).
AAA 2 (BY SIMILARITY).
AAA 3 (BY SIMILARITY).
AAA 4 (BY SIMILARITY).
STALK (BY SIMILARITY).
AAA 5 (BY SIMILARITY).
AAA 6 (BY SIMILARITY).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
E -> L (requires 2 nucleotide substitutions).
/FTid=VAR_013851.
Q -> R.
/FTid=VAR_013852.
S -> C.
/FTid=VAR_013853.
V -> A.
/FTid=VAR_013854.
A -> T.
/FTid=VAR_013855.

FT VARIANT 1640 1640 D -> G.
FT FTid=VAR_013856.
FT VARIANT 2641 2641 S -> N.
FT FTid=VAR_013857.
FT VARIANT 2682 2682 I -> V.
FT FTid=VAR_013858.
FT VARIANT 3004 3004 R -> Q (in PCD; not proven to be pathogenic).
FT FTid=VAR_013859.
FT VARIANT 3474 3474 A -> T.
FT FTid=VAR_013860.
FT VARIANT 3715 3715 L -> V.
FT FTid=VAR_013861.
FT VARIANT 3765 3765 S -> P.
FT FTid=VAR_013862.
FT VARIANT 4177 4177 T -> I.
FT FTid=VAR_013863.
SQ SEQUENCE 4523 AA; 520969 MW; 7C9AT7C95E296B89 CRC64;
Query Match 46.9%; Score 45; DB 1; Length 4523;
Best Local Similarity 50.0%; Pred. No. 97;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 5 FKNQFOTLKIVILG 18
Db 648 FWSNFASLYFLG 661
RESULT 24
SECD_HAEN
ID SECD_HAEN STANDARD; PRT; 616 AA.
AC P44591;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein-export membrane protein secd.
GN SECD OR H10240.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]_taxID=727;
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
RL Science 269:496-512 (1995).
CC -!- FUNCTION: Involved in protein export (By similarity).
CC -!- SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secd, secdB, secdC, secdE, secdF, secdG and secdH (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (By similarity).
CC -!- SIMILARITY: Belongs to the secd/secdF family. SecD family.
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DR EMBL; U32710; AAC21908.1; -.
DR PIR; I64056; I64056.
DR TIGR; H10240; -.
DR InterPro; IPR005791; SecD.
DR InterPro; IPR003335; SecD_SecF.
DR Pfam; PF02355; SecD_SecF_1.
DR PRINTS; PR01755; SECITRNLCASE.
DR TIGRFAMs; TIGR00916; 2A0604801.1.
DR TIGRFAMs; TIGR01129; secD; 1.
DR Protein transport; Translocation; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 453 473 POTENTIAL.
FT TRANSMEM 475 495 POTENTIAL.
FT TRANSMEM 497 517 POTENTIAL.
FT TRANSMEM 562 582 POTENTIAL.
FT TRANSMEM 585 605 POTENTIAL.
SQ SEQUENCE 616 AA; 66986 MW; 7DE1E4B085065F8F CRC64;

Query Match 45.8%; Score 44; DB 1; Length 616;
Best Local Similarity 38.9%; Pred. No. 20;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 SOYQWKNFQTLKIVLG 18
DB 3 NRYPLWKNLWVIFAIG 20

RESULT 25
PYRB MYCPE STANDARD; PRT; 300 AA.
AC QBUX9;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
transcarbamylase) (ATCase).
GN PYRB OR MYPE7890.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=12466555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
+ N-carbamoyl-L-aspartate.
CC -!- PATHWAY: Pyrimidine biosynthesis; second step.
CC -!- SIMILARITY: Belongs to the ATCase/OTCase family.
CC
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CC -----
EMBL; AF004173; BAC44582.1; -.
DR HAMAP; MF 00001; -.
DR InterPro; IPR006130; Asp/Orn Cotransf.
DR InterPro; IPR002082; Asp carbamyltransf.
DR InterPro; IPR006131; OTCase O.
DR InterPro; IPR006132; OTCase P.
DR Pfam; PF00185; OTCase; 1.
DR Pfam; PF02729; OTCase_N; 1.
DR PRINTS; PR00100; AOTCASE.
DR TIGRFAMs; TIGR00670; asp_carb_tr; 1.

DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
KW Pyrimidine biosynthesis; Transferase; Complete proteome.
SQ SEQUENCE 300 AA; 34532 MW; 9F9200EEEDB298E2 CRC64;

Query Match 44.8%; Score 43; DB 1; Length 300;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 YQWKNFQTLKIVLG 18
DB 143 YEKFKSFEGLTAIVG 158

RESULT 26
CKR3 CERAE STANDARD; PRT; 355 AA.
AC P56492;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
(CCR3).
GN CCR3 OR CWKBR3.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Sol N., Treboute C., Gomas E., Ferchal P., Alizon M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin,
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC -----
EMBL; Y13775; CAA74106.1; -.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECF_F2_1; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY
SQ SEQUENCE 355 AA; 40830 MW; 44F7A5E9FEB978FF CRC64;

Query Match 44.8%; Score 43; DB 1; Length 355;
Best Local Similarity 58.3%; Pred. No. 17;

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ENBL; AF017283; AAB70527.1; -.	1	34	EXTRACELLULAR (POTENTIAL).
ENBL; Y13776; CAA74107.1; -.	35	62	1 (POTENTIAL).
InterPro; IPR000276; GPCR_Rhodpsn.	63	72	1 CYTOPLASMIC (POTENTIAL).
Pfam; PF00001; 7tm_1; 1.	73	93	2 (POTENTIAL).
PRINTS; PR00237; GPCRHHODPSN.	94	107	3 (POTENTIAL).
PROSITE; PS0237; G PROTEIN RECP Fl_1; 1.	108	129	EXTRACELLULAR (POTENTIAL).
PROSITE; PS50262; G PROTEIN RECP Fl_2; 1.	130	146	EXTRACELLULAR (POTENTIAL).
SMART; SM00001; G-protein coupled receptor; Transmembrane.	147	171	4 (POTENTIAL).
DOMAIN 1	172	203	5 (POTENTIAL).
TRANSMEM 35	204	223	EXTRACELLULAR (POTENTIAL).
DOMAIN 63	224	239	CYTOPLASMIC (POTENTIAL).
TRANSMEM 73	240	264	6 (POTENTIAL).
DOMAIN 94	265	281	EXTRACELLULAR (POTENTIAL).
TRANSMEM 108	282	305	7 (POTENTIAL).
DOMAIN 130	306	355	CYTOPLASMIC (POTENTIAL).
TRANSMEM 147			
DOMAIN 172			
TRANSMEM 172			
DOMAIN 204			
TRANSMEM 204			
DOMAIN 224			
TRANSMEM 224			
DOMAIN 240			
TRANSMEM 240			
DOMAIN 265			
TRANSMEM 265			
DOMAIN 282			
TRANSMEM 282			
DOMAIN 306			
TRANSMEM 306			

Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).

-1- CATALYTIC ACTIVITY: Tryptophan + O(2) = 5-hydroxytryptophan.

-1- COFACTOR: FAD (Potential).

-1- PATHWAY: Violacein biosynthesis; branch 2; first step.

-1- INDUCTION: By N-acetylhomoserine lactone (AHL).

-1- BIOTECHNOLOGY: Violacein production is used as a biosensor for the detection of quorum-sensing AHL production. Violacein possesses antibacterial, antiviral, antimicrobial, antileishmanial, trypanocidal and potential antitumoral activities.

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EWBL; A212851; AAD51811.1; -
 EMBL; AB032799; BAA84785.1; -
 EMBL; AB016921; AAO60935.1; -
 InterPro; IPR000733; Flav monooxygenase.
 Pfam; PF01360; Monooxygenase; 1.
 PRINTS; PR00420; RNMNOXGNASE.
 Oxidoreductase; Flavoprotein; FAD; Antibiotic biosynthesis;
 Complete proteome.
 NP BIND 2 20 FAD (POTENTIAL).
 FT CONFLICT 31 31 V -> I (IN REF. 1).
 FT CONFLICT 153 153 V -> A (IN REF. 1).
 FT SEQUENCE 373 AA; 41622 MW; 64205F8BCED4BC25 CRC64;

Query Match 44.8%; Score 43; DB 1; Length 373;
 Best Local Similarity 42.9%; Pred. No. 17;
 Matches 9; Conservative 3; Mismatches 1; Indels 8; Gaps 1;

Qy 6 WNFQTL-----KIVILG 18
 Db 248 WNFMTLSHDCRCHDGLVLLG 268

RESULT 29

SRF2_BACSU STANDARD; PRT; 3587 AA.

AC Q04747;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Surfactin synthetase subunit 2.
 GN SRFAB OR SRFAB2 OR COML OR BSU03490.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 [1]
 RN SEQUENCE OF 1-3077 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=93181186; PubMed=8441623;
 RA Fuma S., Fujishima Y., Corbelli N., D'Souza C., Nakano M.M., Zuber P., Yamane K.;
 RA "Nucleotide sequence of 5' portion of srfA that contains the region required for competence establishment in Bacillus subtilis.";
 RL Nucleic Acids Res. 21:93-97 (1993).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RX MEDLINE=93360813; PubMed=8355609;
 RA Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M., Venema G., van Sinderen D.;
 RA "Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis.";
 RT Mol. Microbiol. 8:821-831 (1993).
 [3]
 RN SEQUENCE FROM N.A.

RC STRAIN=168;
 RX MEDLINE=97124189; PubMed=8969502;
 RA Yamane K., Kumano M., Kurita K.;
 RA "The 25 degrees-36 degrees region of the Bacillus subtilis chromosome: determination of the sequence of a 146 kb segment and identification of 113 genes.";
 RT Microbiology 142:3047-3056 (1996).
 [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G., Azavedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruchi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A., Deizot F., Devine K.M., Dutertre A., Ehrlich S.D., Emmerson P.T., Enrian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Parro D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Prascan E., Fujic P., Purnelle B., Porwollik S., Prescott A.M., Rieger M., Rivolta C., Roche E., Roche B., Rose M., Reynolds S., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
 RL Nature 390:249-256 (1997).
 [5]
 RN SEQUENCE OF 514-800 FROM N.A.
 RC STRAIN=ATCC 21332;
 RX MEDLINE=92290255; PubMed=1601288;
 RA Borchert S., Patil S.S., Marahiel M.A.;
 RT "Identification of putative multifunctional peptide synthetase genes using highly conserved oligonucleotide sequences derived from known synthetases.";
 RL FEMS Microbiol. Lett. 71:175-180 (1992).
 CC -1- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, GLU, ASP AND VAL.
 CC ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.
 CC -1- COFACTOR: Contains 3 covalently bound phosphotethines.
 CC -1- PATHWAY: Cyclic peptide antibiotic surfactin biosynthesis.
 CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.
 CC -1- SIMILARITY: Contains 3 acyl carrier domains.
 CC -----
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EWBL; D13262; BAA02523.1; -
 EMBL; X70356; CAA49817.1; -
 EMBL; D50453; BAA08983.1; -
 EMBL; Z99105; CAB12143.1; -
 EMBL; X65835; CAA46678.1; -

DR PIR; I40486; I40486.
DR HGSP; PI4687; LAMU.
DR Subtilist; BG10169; srFAB.
DR InterPro; IPR000873; AMP-bind.
DR InterPro; IPR001242; Condensatn.
DR InterPro; IPR006163; Pp bind.
DR InterPro; IPR006162; Pplantne S.
DR Pfam; PF00501; AMP-binding; 3.
DR Pfam; PF00668; Condensation; 4.
DR Pfam; PF00550; PP-binding; 3.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 3.
DR PROSITE; PS00455; AMP BINDING; 3.
DR PROSITE; PS00075; ACP DOMAIN; 3.
KW Ligase; Antibiotic biogynthesis; Phosphopantetheine; Sporulation;
KW Multifunctional enzyme; Repeat; Complete. Proteome
FT REPEAT ? 1040 DOMAIN 1 (VAL-ACTIVATING).
FT REPEAT ? 2096 DOMAIN 2 (ASP-ACTIVATING).
FT REPEAT ? 3114 DOMAIN 3 (D-LEU-ACTIVATING).
FT DOMAIN 970 1036 ACYL CARRIER (ACP) 1.
FT DOMAIN 2015 2082 ACYL CARRIER (ACP) 2.
FT DOMAIN 3043 3109 ACYL CARRIER (ACP) 3.
FT BINDING 999 999 PHOSPHOPANTHETHEINE (POTENTIAL).
FT BINDING 2045 2045 PHOSPHOPANTHETHEINE (POTENTIAL).
FT BINDING 3073 3073 PHOSPHOPANTHETHEINE (POTENTIAL).
FT CONFLICT 33 33 S -> F (IN REF. 1).
FT CONFLICT 42 42 A -> G (IN REF. 1).
FT CONFLICT 110 110 Q -> D (IN REF. 1).
FT CONFLICT 113 115 RQA -> AOG (IN REF. 1).
FT CONFLICT 139 139 A -> V (IN REF. 1).
FT CONFLICT 259 259 L -> W (IN REF. 1).
FT CONFLICT 309 309 R -> A (IN REF. 1).
FT CONFLICT 478 480 TPA -> SRP (IN REF. 1).
FT CONFLICT 596 596 MISSING (IN REF. 1).
FT CONFLICT 648 648 A -> R (IN REF. 1).
FT CONFLICT 680 682 RHV -> ETL (IN REF. 1).
FT CONFLICT 694 698 EQSIT -> DKRIS (IN REF. 5).
FT CONFLICT 788 788 M -> L (IN REF. 5).
FT CONFLICT 939 940 PL -> LV (IN REF. 1).
FT CONFLICT 1038 1038 N -> I (IN REF. 1).
FT CONFLICT 1133 1133 H -> Q (IN REF. 1).
FT CONFLICT 1310 1310 V -> C (IN REF. 1).
FT CONFLICT 1333 1333 G -> V (IN REF. 1).
FT CONFLICT 1384 1384 P -> R (IN REF. 1).
FT CONFLICT 1582 1582 G -> E (IN REF. 1).
FT CONFLICT 1677 1682 KRADG -> E (IN REF. 1).
FT CONFLICT 1700 1700 C -> S (IN REF. 1).
FT CONFLICT 1755 1755 F -> K (IN REF. 1).
FT CONFLICT 1787 1787 T -> S (IN REF. 1).
FT CONFLICT 1801 1822 GAIAGRDYDPEDAFAKEPTTG -> APSPGGLICMGRCIC
ETPDNR (IN REF. 1).
FT CONFLICT 1915 1916 LG -> PK (IN REF. 1).
FT CONFLICT 2075 2075 R -> C (IN REF. 1).
FT CONFLICT 2079 2079 A -> V (IN REF. 1).
FT CONFLICT 2141 2145 ARLTP -> LRSLN (IN REF. 1).
FT CONFLICT 2445 2445 E -> Q (IN REF. 1).
FT CONFLICT 2485 2489 ATDLF -> RQICS (IN REF. 1).
FT CONFLICT 2546 2566 TVHOLFETVQRKHDPATV -> DGCISYSKRLLSATKT
ARLSHT (IN REF. 1).
FT CONFLICT 2615 2615 MSAVLGV -> KCPRCAS (IN REF. 1).
FT CONFLICT 2644 2645 KL -> NV (IN REF. 1).
FT CONFLICT 2713 2713 D -> H (IN REF. 1).
FT CONFLICT 2723 2723 D -> H (IN REF. 1).
FT CONFLICT 2876 2881 GELCVA -> RALRG (IN REF. 1).
FT CONFLICT 2899 2900 RF -> L (IN REF. 1).
FT CONFLICT 2958 2960 EDR -> ODA (IN REF. 1).
FT CONFLICT 2964 2964 R -> A (IN REF. 1).
SQ SEQUENCE 3587 AA; 401248 MW; 6B0B5A9FF32054D CRC64;

Query Match 44.8%; Score 43; DB 1; Length 3587;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVLG 18
DB 1751 ASFAFDANFESLRIVLG 1768
RESULT 30
UTR4 YEAST STANDARD; PRT; 241 AA.
AC P32626;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE UTR4 protein (Unknown transcript 4 protein).
GN UTR4 OR YEL038W OR SYGP-ORF20.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313264; PubMed=9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Moesdale D., Nakahara K., Namath A., Norgren R., Oefner P.,
RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V";
RL Nature 387:78-81 (1997).
RN [2]
RP SEQUENCE OF 1-158 FROM N.A.
RC STRAIN=B-6441;
RX MEDLINE=94016558; PubMed=8411151;
RA Melnick L., Sherman F.;
RT "The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
RT J. Mol. Biol. 233:372-388 (1993).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L22173; AAA34939.1; -;
DR EMBL; S65964; AAD13973.1; -;
DR EMBL; S66121; AAB28443.1; -;
DR EMBL; U18779; AAB65004.1; -;
DR PIR; S30843; S30843.
DR Germonline; 139042; -;
DR SGD; S0000764; UTR4.
DR InterPro; IPR005834; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
FT CONFLICT 70 71 ID -> MH (IN REF. 2).
FT CONFLICT 153 158 AHDSLD -> GMIRMT (IN REF. 2).
SQ SEQUENCE 241 AA; 26735 MW; BF6FBBC7FB14B5AD CRC64;
Query Match 43.8%; Score 42; DB 1; Length 241;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 QYQFWKFNQTL 12
DB 231 KYQVKNFETL 241

Search completed: March 4, 2004, 18:00:06
JOB time : 9.07755 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 29.0204 Seconds
(without alignments)
195.701 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQQFWKNFQPLKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phase: *
10: sp_plant: *
11: sp_rident: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	52	4	Q9P1T5
2	96	100.0	60	4	Q9P1T4
3	96	100.0	333	4	O14694
4	96	100.0	334	6	Q9TUQ7
5	96	100.0	339	4	Q9UN24
6	96	100.0	339	4	Q9UN26
7	96	100.0	339	4	Q9UN23
8	96	100.0	339	4	Q9UBJ7
9	96	100.0	339	4	Q9UN25
10	96	100.0	339	4	Q9UN27
11	96	100.0	339	4	Q9UBT9
12	96	100.0	339	4	Q9UN28
13	96	100.0	339	6	Q9TQW0
14	96	100.0	339	6	Q9TUX1
15	96	100.0	339	6	Q9TUU9
16	96	100.0	339	6	Q9TUW9

17	96	100.0	339	6	Q9TS01
18	96	100.0	339	6	Q9TU08
19	96	100.0	339	6	Q9TQW4
20	96	100.0	339	6	Q9TUW4
21	96	100.0	339	6	Q9TU07
22	96	100.0	339	6	Q9TUR6
23	96	100.0	339	6	Q9TQV6
24	96	100.0	339	6	Q9TUW6
25	96	100.0	339	6	Q9TU09
26	96	100.0	339	6	Q9TUR2
27	96	100.0	339	6	Q9TQV0
28	96	100.0	339	6	Q9TU05
29	96	100.0	339	6	Q9TUS7
30	96	100.0	339	6	Q9TUM3
31	96	100.0	339	6	Q9TUS5
32	96	100.0	339	6	Q9TQV2
33	96	100.0	339	6	Q9TQV3
34	96	100.0	339	6	Q9TU08
35	96	100.0	339	6	Q9TUR3
36	96	100.0	339	6	Q9TQW2
37	96	100.0	339	6	Q9TDX2
38	96	100.0	339	6	Q9TS04
39	96	100.0	339	6	Q9TQK2
40	96	100.0	339	6	Q9TSQ3
41	96	100.0	339	6	Q9TUR0
42	96	100.0	339	6	Q9TUM5
43	96	100.0	339	6	Q9TUQ4
44	96	100.0	339	6	Q9TU06
45	96	100.0	339	6	Q9TUR8
46	96	100.0	339	6	Q9TUS8
47	96	100.0	339	6	Q9TUR7
48	96	100.0	339	6	Q9TU04
49	96	100.0	339	6	Q9TU06
50	96	100.0	339	6	Q9TUX0
51	96	100.0	339	6	Q9TUR8
52	96	100.0	339	6	Q9TUR1
53	96	100.0	339	6	Q9TUS9
54	96	100.0	344	6	Q9TQK8
55	96	100.0	344	6	O77833
56	96	100.0	352	6	Q9TSK1
57	96	100.0	352	6	Q9SNC5
58	96	100.0	352	6	Q9TV49
59	96	100.0	352	6	Q9XT14
60	96	100.0	352	6	Q9XT76
61	96	100.0	352	6	Q9SNC3
62	96	100.0	352	6	O18771
63	96	100.0	352	6	Q9TV47
64	96	100.0	352	6	Q9SNC1
65	96	100.0	352	6	O18772
66	96	100.0	352	6	Q9SNC6
67	96	100.0	352	6	Q9SNC8
68	96	100.0	352	6	Q9SNC7
69	96	100.0	352	6	Q9SNC0
70	96	100.0	352	6	Q9BGN5
71	96	100.0	352	6	Q9TV42
72	96	100.0	352	6	Q9XT13
73	96	100.0	352	6	O77776
74	96	100.0	352	6	Q9MZA3
75	96	100.0	352	6	Q9TSQ7
76	96	100.0	352	6	Q9MZA2
77	96	100.0	352	6	Q9TV50
78	96	100.0	352	6	Q9XS99
79	96	100.0	352	6	Q9TV45
80	96	100.0	352	6	Q9SNE1
81	96	100.0	352	6	Q9BGN6
82	96	100.0	352	6	Q9SND0
83	96	100.0	352	6	Q9T962
84	96	100.0	352	6	Q9TV43
85	96	100.0	352	6	Q9SNE8
86	93	96.9	339	6	Q9TUT4
87	93	96.9	339	6	Q9TU03
88	93	96.9	339	6	Q9TUR9
89	93	96.9	339	6	Q9TQTO

Q9tsq1 cercopithec
Q9tnu8 cercopithec
Q9tqw4 pan troglod
Q9tuw4 pan troglod
Q9tq7 cercopithec
Q9tur6 cercopithec
Q9tq6 colobus gue
Q9tuw6 pan troglod
Q9tuq9 cercopithec
Q9tur2 erythrocebu
Q9tq0 papio papio
Q9tu5 cercopithec
Q9tus7 papio papio
Q9tuw3 pongo pygma
Q9tus5 papio papio
Q9tq2 papio papio
Q9tq3 cercopithec
Q9tu8 cercopithec
Q9tur3 erythrocebu
Q9tq2 pongo pygma
Q9tq2 erythrocebu
Q9tsq4 cercopithec
Q9tq2 gorilla gor
Q9tsq3 cercopithec
Q9tur0 cercopithec
Q9tu5 pan troglod
Q9tu4 erythrocebu
Q9tu6 erythrocebu
Q9tus8 papio papio
Q9tus6 papio papio
Q9tur7 cercopithec
Q9tu4 cercopithec
Q9tu6 cercopithec
Q9tux0 hylobates c
Q9tur8 cercopithec
Q9tus9 papio papio
Q9tq8 cercocebus
Q9tq3 cercocebus
Q9tq1 cercopithec
Q9tq5 cercocebus s
Q9tq4 cercocebus
Q9xt14 colobus gue
Q9xt76 cercopithec
Q9snc3 miopithecus
Q9t771 pan troglod
Q9tv47 cercopithec
Q9snc1 theropithec
Q9t772 pan troglod
Q9snc6 trachypithe
Q9snc8 colobus pol
Q9snc7 nasalis lar
Q9snc0 hylobates m
Q9bgn5 cercopithec
Q9tv42 cercopithec
Q9xt13 papio amibi
Q9t776 cercocebus
Q9mza3 hylobates a
Q9tsq7 cercopithec
Q9mza2 cercopithec
Q9tv50 pan troglod
Q9xs99 gorilla gor
Q9tv45 cercopithec
Q9sne1 cercocebus
Q9bgn6 cercopithec
Q9snc0 erythrocebu
Q9t962 pygathrix a
Q9tv43 cercopithec
Q9sne8 cercopithec
Q9tut4 macaca neme
Q9tu3 macaca mula
Q9tur9 saquinus sp
Q9tq0 macaca fasc

90 93 96.9 339 6 Q9TUT9
 91 93 96.9 339 6 Q9TSN2
 92 93 96.9 339 6 Q9TSN3
 93 93 96.9 339 6 Q9TUT7
 94 93 96.9 339 6 Q9TUT6
 95 93 96.9 339 6 Q9TUT6
 96 93 96.9 339 6 Q9TUT0
 97 93 96.9 339 6 Q9TUT1
 98 93 96.9 339 6 Q9TUT0
 99 93 96.9 339 6 Q9TUT0
 100 93 96.9 339 6 Q9TUT1

ALIGNMENTS

RESULT 1
 Q9P1T5 PRELIMINARY; PRT; 52 AA.
 ID Q9P1T5
 AC Q9P1T5
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mutant chemokine receptor CCR5 (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99392755; PubMed=10465086;
 RA Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
 RA Bond V.C.;
 RT "Characterization of a third CCR5 amplicon from CCR5-delta32-
 heterozygous HIV-1-infected individuals.";
 RL AIDS 13:1585-1586(1999).
 DR EMBL; AF056019; AAF65578.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON TER 1 1
 FT VARIANT 41 41 P->S
 SQ SEQUENCE 52 AA; 5962 MW; DAEB2A5A9529C3A9 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
 Db 11 SQYQFWKNFQTLKIVILG 28

RESULT 2
 Q9P1T4 PRELIMINARY; PRT; 60 AA.
 ID Q9P1T4
 AC Q9P1T4
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Chemokine receptor CCR5 (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99392755; PubMed=10465086;
 RA Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,
 RA Bond V.C.;
 RT "Characterization of a third CCR5 amplicon from CCR5-delta32-
 heterozygous HIV-1-infected individuals.";

RL AIDS 13:1585-1586(1999).
 DR EMBL; AF056020; AAF65579.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON TER 1 1
 FT NON TER 60 60
 SQ SEQUENCE 60 AA; 7156 MW; AFF4B9CAF6B80AFB CRC64;

Query Match 100.0%; Score 96; DB 4; Length 60;
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
 Db 11 SQYQFWKNFQTLKIVILG 28

RESULT 3
 O14694 PRELIMINARY; PRT; 333 AA.
 ID O14694
 AC O14694
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CCR5 receptor (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
 DR EMBL; AF011504; AAB65704.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON TER 333 333
 SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 96; DB 4; Length 333;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
 Db 166 SQYQFWKNFQTLKIVILG 183

RESULT 4
 Q9TUT7 PRELIMINARY; PRT; 334 AA.
 ID Q9TUT7
 AC Q9TUT7
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).

GN CCR5.
 OS Erythrocebus patas (Red guenon) (Hussar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Erythrocebus.
 OX NCBI_TaxID=9538;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162049; AAD47804.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 334 334
 SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;
 Query Match 100.0%; Score 96; DB 6; Length 334;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SQYQFWKNFQTLKIVILG 18
 Db 173 SQYQFWKNFQTLKIVILG 190
 RESULT 5
 Q9UN24 PRELIMINARY; PRT; 339 AA.
 AC Q9UN24;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161919; AAD47676.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;
 Query Match 100.0%; Score 96; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SQYQFWKNFQTLKIVILG 18
 Db 178 SQYQFWKNFQTLKIVILG 195
 RESULT 6
 Q9UN26 PRELIMINARY; PRT; 339 AA.
 AC Q9UN26;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161919; AAD47673.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE529F4B CRC64;
 Query Match 100.0%; Score 96; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SQYQFWKNFQTLKIVILG 18
 Db 178 SQYQFWKNFQTLKIVILG 195
 RESULT 7
 Q9UN23 PRELIMINARY; PRT; 339 AA.
 AC Q9UN23;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161920; AAD47677.1; -.
 Query Match 100.0%; Score 96; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
Db 178 SQYQWKNFQTLKIVILG 195

RESULT 8
Q9UBJ7
ID Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFF1E2P27A CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
Db 178 SQYQWKNFQTLKIVILG 195

RESULT 9
Q9UN25
ID Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFF1E2P27A CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
Db 178 SQYQWKNFQTLKIVILG 195

RESULT 10
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161918; AAD47675.1; -.
DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
Db 178 SQYQWKNFQTLKIVILG 195

RESULT 10
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO: 00016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

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Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 11
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F47 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 12
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F47 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 13
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match      100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

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RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match      100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

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RESULT 13
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match      100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

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RESULT 13
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match      100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

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DR	DR	DR	DR
GO;	Int	Pfa	

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OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; AAD47778.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT SEQUENCE 339 AA; 33216 MW; 847E935FA03B52D CRC64;
SQ
Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195
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|||||

RESULT 18
Q9TU08 PRELIMINARY; PRT; 339 AA.
ID Q9TU08
AC Q9TU08
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT SEQUENCE 339 AA; 33049 MW; 6D1A93F66270F3ED CRC64;
SQ
Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195
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|||||

RESULT 19
Q9TQW4 PRELIMINARY; PRT; 339 AA.
ID Q9TQW4
AC Q9TQW4
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT SEQUENCE 339 AA; 39129 MW; 4A98F8B601D46A4 CRC64;
SQ
Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195
|||||
|||||

RESULT 20
Q9TUM4 PRELIMINARY; PRT; 339 AA.
ID Q9TUM4
AC Q9TUM4
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
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|||||
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DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
DR NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 8E699882BAC0E84 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
DB 178 SQYQWKNFQTLKIVILG 195

RESULT 21
Q9TUR6
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
DE CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
DR NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 847D5F92BB03E652 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
DB 178 SQYQWKNFQTLKIVILG 195

RESULT 22
Q9TUR6
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
DE CCR5.
OS Cercopithecus nictitans (White-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
DR NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 847D5F92BB03E652 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
DB 178 SQYQWKNFQTLKIVILG 195

RESULT 23
Q9TUR6
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
DE CCR5.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -.
DR EMBL; AF162000; AAD47755.1; -.
DR EMBL; AF162001; AAD47756.1; -.
DR EMBL; AF162002; AAD47757.1; -.
DR EMBL; AF162003; AAD47758.1; -.
DR EMBL; AF162004; AAD47759.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0004872; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.
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DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
DB 178 SOYQFWKNFQTLKIVILG 195

RESULT 24
Q9TUW6 PRELIMINARY; PRT; 339 AA.
AC Q9TUW6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161900; AAD47657.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5M4 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
DB 178 SOYQFWKNFQTLKIVILG 195

RESULT 25
Q9TUQ9 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus mona.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162041; AAD47796.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF11F3ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
DB 178 SOYQFWKNFQTLKIVILG 195

RESULT 26
Q9TUR2 PRELIMINARY; PRT; 339 AA.
AC Q9TUR2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OC Erythrocebus patas (Red guenon) (Husar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162034; AAD47789.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39138 MW; AD31455EBBC69499 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SQYQFWKNTQTLKIVILG 18
Db 178 SQYQFWKNTQTLKIVILG 195

RESULT 27
Q9TQV0
ID Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161989; AAD47744.1; -.
DR EMBL; AF161988; AAD47743.1; -.
DR GO; GO:0006021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39113 MW; 7F9803EAE0AF9ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNTQTLKIVILG 18
Db 178 SQYQFWKNTQTLKIVILG 195

RESULT 28
Q9TQV0
ID Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";

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RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162046; AAD47801.1; -.
DR EMBL; AF162043; AAD47798.1; -.
DR GO; GO:0006021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39178 MW; 847F8F936B00B6E2 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNTQTLKIVILG 18
Db 178 SQYQFWKNTQTLKIVILG 195

RESULT 29
Q9TQV0
ID Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161995; AAD47750.1; -.
DR GO; GO:0006021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39068 MW; 84EB018085DC0A62 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNTQTLKIVILG 18
Db 178 SQYQFWKNTQTLKIVILG 195

RESULT 30
Q9TQV0
ID Q9TQV0 PRELIMINARY; PRT; 339 AA.

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AC 09TUM3;
DT 01-MAY-2003 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161908; AAD47665.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

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Search completed: March 4, 2004, 18:02:55
 Job time : 29.0204 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:55:22 ; Search time 11.5714 Seconds
(without alignments)
80.307 Million cell updates/sec

Title: US-10-084-813-13
Perfect score: 96
Sequence: 1 SQYFWKNFQTLKIVILG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pgp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pgp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pgp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pgp.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pgp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pgp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	96	100.0	54	4	US-08-833-752-11
2	96	100.0	352	3	US-08-466-343D-2
3	96	100.0	352	3	US-08-087-232A-13
4	96	100.0	352	3	US-08-861-105-14
5	96	100.0	352	3	US-08-575-967A-2
6	96	100.0	352	3	US-09-045-583-52
7	96	100.0	352	4	US-09-517-605-5
8	96	100.0	352	4	US-09-534-185-51
9	96	100.0	352	4	US-08-833-752-5
10	96	100.0	352	4	US-09-502-783A-2
11	96	100.0	352	4	US-09-796-202-1
12	82	85.4	21	3	US-08-907-468-11
13	74	77.1	354	4	US-08-724-984A-2
14	47	49.0	355	4	US-09-886-319A-13
15	45	46.9	355	3	US-09-045-583-53
16	45	46.9	355	4	US-09-534-185-53
17	43.5	45.3	352	4	US-09-489-039A-13500
18	43	44.8	172	4	US-09-621-976-4131
19	43	44.8	344	3	US-08-681-192-2
20	42	43.8	460	4	US-08-935-263-4
21	42	43.8	460	4	US-09-594-185-4
22	42	43.8	727	4	US-09-540-236-3023
23	41	42.7	160	4	US-09-328-352-6593
24	41	42.7	255	4	US-09-491-577-2
25	41	42.7	363	4	US-09-252-991A-25052
26	40	41.7	254	4	US-09-134-001C-4582
27	40	41.7	311	4	US-09-134-001C-5171

28	40	41.7	316	4	US-09-489-039A-8904
29	40	41.7	355	1	US-08-012-988A-2
30	40	41.7	355	1	US-08-450-393A-5
31	40	41.7	355	3	US-08-446-669-5
32	40	41.7	355	4	US-09-239-938-1
33	40	41.7	355	4	US-08-833-752-9
34	40	41.7	355	4	US-09-886-319A-14
35	40	41.7	355	5	PCT-US95-00476-5
36	40	41.7	371	3	US/08/622
37	40	41.7	371	4	US-09-165-922A-10
38	40	41.7	659	4	US-09-252-991A-26013
39	40	41.7	2037	4	US-09-543-681A-5538
40	39	40.6	92	4	US-09-328-352-5171
41	39	40.6	448	4	US-09-134-000C-3794
42	39	40.6	452	4	US-09-530-836-6
43	39	40.6	485	4	US-09-134-000C-6031
44	39	40.6	598	2	US-08-853-659A-53
45	39	40.6	684	4	US-09-377-497-70
46	39	40.6	690	3	US-09-422-869-28
47	38	39.6	87	4	US-09-134-000C-6145
48	38	39.6	135	4	US-09-171-461-24
49	38	39.6	212	4	US-09-489-039A-9275
50	38	39.6	243	4	US-09-107-532A-4908
51	38	39.6	277	4	US-09-134-000C-4158
52	38	39.6	320	4	US-09-252-991A-30676
53	38	39.6	389	4	US-09-491-577-52
54	38	39.6	576	4	US-09-543-681A-4990
55	38	39.6	879	1	US-08-306-546C-2
56	38	39.6	879	2	US-08-530-524A-2
57	37	38.5	74	4	US-09-328-352-4234
58	37	38.5	105	4	US-09-732-210-130
59	37	38.5	118	1	US-08-226-264-23
60	37	38.5	138	4	US-09-134-001C-4441
61	37	38.5	182	1	US-08-226-264-28
62	37	38.5	216	3	US-08-924-747-12
63	37	38.5	216	3	US-09-247-373B-12
64	37	38.5	216	3	US-09-296-715-12
65	37	38.5	219	3	US-08-924-747-20
66	37	38.5	219	3	US-09-247-373B-20
67	37	38.5	219	3	US-09-296-715-20
68	37	38.5	248	6	5169835-15
69	37	38.5	283	4	US-09-134-000C-6045
70	37	38.5	329	4	US-09-328-352-6027
71	37	38.5	329	4	US-09-502-783A-9
72	37	38.5	344	3	US-08-466-343D-9
73	37	38.5	347	1	US-08-461-244-3
74	37	38.5	360	1	US-08-450-393A-4
75	37	38.5	360	3	US-08-446-669-4
76	37	38.5	360	3	US-09-045-583-50
77	37	38.5	360	3	US-09-045-583-51
78	37	38.5	360	3	US-09-534-185-50
79	37	38.5	360	4	US-09-534-185-51
80	37	38.5	360	4	US-08-833-752-7
81	37	38.5	360	4	US-09-131-827A-2
82	37	38.5	360	4	US-09-131-827A-20
83	37	38.5	360	5	PCT-US95-00476-4
84	37	38.5	374	1	US-08-450-393A-2
85	37	38.5	374	3	US-08-446-669-2
86	37	38.5	374	5	PCT-US95-00476-2
87	37	38.5	380	4	US-09-489-039A-13215
88	37	38.5	454	4	US-09-134-001C-3547
89	37	38.5	615	3	US-09-462-844-3
90	37	38.5	615	4	US-09-899-482-3
91	37	38.5	731	1	US-09-014-897-2
92	37	38.5	731	1	US-08-731-716-2
93	37	38.5	2233	2	US-08-569-853-1
94	37	38.5	2233	2	US-08-569-853-2
95	37	38.5	2233	3	US-08-967-433-1
96	36	37.5	69	4	US-09-673-395A-358
97	36	37.5	96	4	US-09-107-532A-5808
98	36	37.5	108	4	US-09-107-532A-7196
99	36	37.5	113	4	US-09-543-681A-8228
100	36	37.5	139	4	US-09-540-236-3184

Sequence 8904, Ap
Sequence 2, Appli
Sequence 5, Appli
Sequence 5, Appli
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Sequence 10, Appli
Sequence 26013, A
Sequence 5538, Ap
Sequence 5171, Ap
Sequence 3794, Ap
Sequence 6, Appli
Sequence 6031, Ap
Sequence 53, Appli
Sequence 70, Appli
Sequence 28, Appli
Sequence 6145, Ap
Sequence 24, Appli
Sequence 9275, Ap
Sequence 4908, Ap
Sequence 4158, Ap
Sequence 30676, A
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Sequence 4990, Ap
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Sequence 20, Appli
Patent No. 5169835
Sequence 6045, Ap
Sequence 6027, Ap
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Sequence 2, Appli
Sequence 13215, A
Sequence 3547, Ap
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 358, App
Sequence 5808, Ap
Sequence 7196, Ap
Sequence 8228, Ap
Sequence 3184, Ap

ALIGNMENTS

```

RESULT 1
US-08-833-752-11
; Sequence 11, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-833-752-11
Query Match 100.0%; Score 96; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | |
Db 9 SQYQFWKNFQTLKIVILG 26

RESULT 2
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-466-343D-2
Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 3
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-087-232A-13

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Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 4
US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-861-105-14

Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 5
US-08-575-967A-2
; Sequence 2, Application US/08575967A
; Patent No. 6265184
; GENERAL INFORMATION:
; APPLICANT: Gray et al.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/575,967A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6265184 and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32918
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-485-1900
; TELEFAX: 206-485-1662
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; US-08-575-967A-2

Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 6
US-09-045-583-52
; Sequence 52, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/045,583
 ; FILING DATE: 20-MAR-98
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MNI-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 52:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; US-09-045-583-52

Query Match 100.0%; Score 96; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 7
 US-09-517-605-5
 ; Sequence 5, Application US/09517605
 ; Patent No. 6391567
 ; GENERAL INFORMATION:
 ; APPLICANT: Littman, Dan R.
 ; APPLICANT: Kwon, Douglas S.
 ; APPLICANT: van Kooyk, Yvette
 ; APPLICANT: Geijzenbeck, Ineo
 ; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
 ; TITLE OF INVENTION: CELLS
 ; FILE REFERENCE: 1049-1-017
 ; CURRENT APPLICATION NUMBER: US/09/517,605
 ; CURRENT FILING DATE: 2000-03-02
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 352
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-517-605-5

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 8
 US-09-534-185-52
 ; Sequence 52, Application US/09534185
 ; Patent No. 6403767
 ; GENERAL INFORMATION:
 ; APPLICANT: Graham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
 ; Heparin-binding Receptor Superfamily and Uses
 ; Therefor
 ; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/534,185
 ; FILING DATE: 24-Mar-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/045,583
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MNI-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 52:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
 ; US-09-534-185-52

Query Match 100.0%; Score 96; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 9
 US-08-833-752-5
 ; Sequence 5, Application US/08833752
 ; Patent No. 6448375
 ; GENERAL INFORMATION:
 ; APPLICANT: SAMSON, MICHEL
 ; APPLICANT: PARMENTIER, MARC
 ; APPLICANT: VASSART, GILBERT
 ; APPLICANT: LIBERT, FREDERICK
 ; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
 ; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe, Martens, Olson & Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,752
 ; FILING DATE: 9-APR-1997
 ; CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-752-5

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 10
US-09-502-783A-2
Sequence 2, Application US/09502783A
Patent No. 6511826
GENERAL INFORMATION:
APPLICANT: Li, Yi
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
FILE REFERENCE: HDGRL10
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 11
US-09-796-202-1
Sequence 1, Application US/09796202
Patent No. 6548636
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 2048/61010/JPM/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 96; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKFNQTLKIVILG 18
DB 185 SOYQFWKFNQTLKIVILG 202

RESULT 12
US-08-907-468-11
Sequence 11, Application US/08907468
Patent No. 6057102
GENERAL INFORMATION:
APPLICANT: Landau, Nathaniel R.
APPLICANT: Koup, Richard A.
APPLICANT: Liu, Rong
APPLICANT: Paxton, William
TITLE OF INVENTION: HIV CORECEPTOR MUTANTS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,468
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-005 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-907-468-11

Query Match 85.4%; Score 82; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIV 15
DB 7 SOYQFWKFNQTLKIV 21

RESULT 13
US-08-724-984A-2
Sequence 2, Application US/08724984A
Patent No. 638055
GENERAL INFORMATION:
APPLICANT: Derk Bergsma, Mary Brawner, and Uman Shabon
TITLE OF INVENTION: No. 638055el Mouse Genomic Clone of the CC-
TITLE OF INVENTION: CCR5 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,984A
FILING DATE: October 3, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-724-984A-2

Query Match 77.1%; Score 74; DB 4; Length 354;
Best Local Similarity 76.5%; Pred. No. 0.00017;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQYQFWNFQTLKIVIL 17
DB 187 TOYHFWKSFQTLKIVIL 203

RESULT 14
US-09-886-319A-13
Sequence 13, Application US/09886319A
Patent No. 6586185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Joern-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: the Diagnosis and for the Identification of Pharmacologically
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
TITLE OF INVENTION: Active Substances
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 355
TYPE: PRT
ORGANISM: Mus musculus
US-09-886-319A-13

Query Match 49.0%; Score 47; DB 4; Length 355;
Best Local Similarity 61.5%; Pred. No. 5;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
DB 195 WKRFOALKNLILG 207

RESULT 15
US-09-045-583-53
Sequence 53, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-Mar-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-53

Query Match 46.9%; Score 45; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YQFWNFQTLKIVILG 18
DB 192 FQWKLFOALKNLILG 207

RESULT 16
US-09-534-185-53
Sequence 53, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

```

; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-534-185-53

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Query Match 46.9%; Score 45; DB 4; Length 355;
Best Local Similarity 50.0%; Pred. NO. 11;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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QY 3 YQWKNFQTLKIVILG 18
Db 192 FQWKLQALKINLFG 207

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RESULT 17
US-09-489-039A-13500
; Sequence 13500, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13500
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13500

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Query Match 45.3%; Score 43.5; DB 4; Length 352;
Best Local Similarity 43.5%; Pred. NO. 19;
Matches 10; Conservative 3; Mismatches 3; Indels 7; Gaps 1;

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QY 2 QYQFW-----KQFQTLKIVIL 17
Db 196 QLRFWQAGSLDIRTLQTLKIVLL 218

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RESULT 18
US-09-621-976-4131
; Sequence 4131, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:

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; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4131
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -30...-1
; US-09-621-976-4131

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Query Match 44.8%; Score 43; DB 4; Length 172;
Best Local Similarity 57.1%; Pred. NO. 11;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 4 QPWNFQTLKIVIL 17
Db 74 EFRKNFETLRIDVL 87

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RESULT 19
US-08-681-192-2
; Sequence 2, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGSMAN, DERK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFD578
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,192
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

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; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-681-192-2

Query Match 44.8%; Score 43; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FWNKFNQTLKIVI 16
|:|:|:|:|:|:|
Db 195 FWNKFNQTLKIVI 206

RESULT 20
US-08-935-263-4
; Sequence 4, Application US/08935263A
; Patent No. 6117669
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuva
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/08/935,263A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: EP 96115540.5
; EARLIER FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-08-935-263-4

Query Match 43.8%; Score 42; DB 3; Length 460;
Best Local Similarity 54.5%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YQFWKFNQTLK 13
|:|:|:|:|:|:|
Db 127 YQFWKFNQTLK 137

RESULT 21
US-09-594-185-4
; Sequence 4, Application US/09594185
; Patent No. 6365388
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuva
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/09/594,185
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 08/935,263
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: EP 96115540.5
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-09-594-185-4

Query Match 43.8%; Score 42; DB 4; Length 460;
Best Local Similarity 54.5%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YQFWKFNQTLK 13
|:|:|:|:|:|:|
Db 127 YQFWKFNQTLK 137

RESULT 22
US-09-540-236-3023
; Sequence 3023, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3023
; LENGTH: 727
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-3023

Query Match 43.8%; Score 42; DB 4; Length 727;
Best Local Similarity 37.5%; Pred. No. 74;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 YQFWKFNQTLK 17
|:|:|:|:|:|:|
Db 167 YQFWKFNQTLK 182

RESULT 23
US-09-328-352-6593
; Sequence 6593, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6593
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6593

Query Match 42.7%; Score 41; DB 4; Length 160;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YQFWKFNQ 10
|:|:|:|:|:|
Db 146 YQFWKFNQ 153

RESULT 24
US-09-491-577-2
; Sequence 2, Application US/09491577
; Patent No. 6610511
; GENERAL INFORMATION:
; APPLICANT: Yale University
; APPLICANT: Carlson, John R.
; APPLICANT: Kim, Hunhyong
; APPLICANT: Clyne, Peter J.
; APPLICANT: Mair, Coral G.
```

; TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila
 ; FILE REFERENCE: 44574-5061-US
 ; CURRENT APPLICATION NUMBER: US/09/491,577
 ; CURRENT FILING DATE: 2000-01-25
 ; EARLIER APPLICATION NUMBER: US 60/117,132
 ; EARLIER FILING DATE: 1999-01-25
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 255
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-491-577-2

Query Match 42.7%; Score 41; DB 4; Length 255;
 Best Local Similarity 53.3%; Pred. No. 35;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQWKNFQTLKIVIL 17
 Db 48 YKLWSTFTLLIFIL 62

RESULT 25

US-09-252-991A-25052
 ; Sequence 25052, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25052
 ; LENGTH: 363
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25052

Query Match 42.7%; Score 41; DB 4; Length 363;
 Best Local Similarity 60.0%; Pred. No. 51;
 Matches 9; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 4 QFWKNFQTLKIVILG 18
 Db 237 KFWKHQ---VILG 247

RESULT 26

US-09-134-001C-4582
 ; Sequence 4582, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 4582
 ; LENGTH: 254
 ; TYPE: PRT

Query Match 41.7%; Score 40; DB 4; Length 316;
 Best Local Similarity 61.5%; Pred. No. 64;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
 Db 226 MINVOGLKVEILG 238

RESULT 29

; ORGANISM: staphylococcus epidermidis
 US-09-134-001C-4582

Query Match 41.7%; Score 40; DB 4; Length 254;
 Best Local Similarity 53.8%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLK 13
 Db 9 SQYPLWNLQTLK 21

RESULT 27

US-09-134-001C-5171
 ; Sequence 5171, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 5171
 ; LENGTH: 311
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-5171

Query Match 41.7%; Score 40; DB 4; Length 311;
 Best Local Similarity 38.5%; Pred. No. 63;
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
 Db 271 WPNFATILWVVG 283

RESULT 28

US-09-039A-8904
 ; Sequence 8904, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 8904
 ; LENGTH: 316
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-8904

Query Match 41.7%; Score 40; DB 4; Length 316;
 Best Local Similarity 61.5%; Pred. No. 64;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18
 Db 226 MINVOGLKVEILG 238

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US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-012-988A-2

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Query Match 41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy 6 WKNFQTLKIVILG 18
Db 195 WKLFQALKNLFG 207

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```

RESULT 30
US-08-450-393A-5
; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Chargo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A

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; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Czeiz, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-450-393A-5

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Query Match 41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy 6 WKNFQTLKIVILG 18
Db 195 WKLFQALKNLFG 207

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Search completed: March 4, 2004, 18:05:14
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 18:03:03 ; Search time 24.0612 Seconds
(without alignments)
157.962 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQYQFWKFNQTLKIVILG 18

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	96	100.0	18	14	US-10-084-813-77
3	96	100.0	54	9	US-09-938-719-11
4	96	100.0	54	9	US-09-938-226-11
5	96	100.0	54	9	US-09-938-703-11
6	96	100.0	352	9	US-09-725-285-2
7	96	100.0	352	9	US-09-759-841-2
8	96	100.0	352	9	US-09-779-879A-2
9	96	100.0	352	9	US-09-779-879A-22
10	96	100.0	352	9	US-09-779-880A-2
11	96	100.0	352	9	US-09-779-880A-22
12	96	100.0	352	9	US-09-813-653-15
13	96	100.0	352	9	US-09-813-653-17
14	96	100.0	352	9	US-09-796-202-1
15	96	100.0	352	9	US-09-195-662A-2

16	96	100.0	352	9	US-09-339-912A-2	Sequence 2, Appli
17	96	100.0	352	9	US-09-938-719-5	Sequence 5, Appli
18	96	100.0	352	9	US-09-938-226-5	Sequence 5, Appli
19	96	100.0	352	9	US-09-938-703-5	Sequence 5, Appli
20	96	100.0	352	9	US-09-502-783A-2	Sequence 2, Appli
21	96	100.0	352	10	US-09-734-221A-14	Sequence 14, Appli
22	96	100.0	352	11	US-09-826-509-477	Sequence 477, App
23	96	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
24	96	100.0	352	14	US-10-232-686-2	Sequence 2, Appli
25	96	100.0	352	14	US-10-086-814-1	Sequence 1, Appli
26	96	100.0	352	14	US-10-067-800-2	Sequence 2, Appli
27	96	100.0	352	14	US-10-067-800-22	Sequence 22, Appli
28	96	100.0	352	14	US-10-290-058A-6	Sequence 6, Appli
29	96	100.0	352	14	US-10-225-567A-352	Sequence 352, App
30	96	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
31	96	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
32	96	100.0	352	14	US-10-164-643-52	Sequence 52, Appli
33	96	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
34	96	100.0	352	14	US-10-135-839-2	Sequence 2, Appli
35	96	100.0	352	14	US-10-135-839-22	Sequence 22, Appli
36	96	100.0	352	14	US-10-239-423-67	Sequence 67, Appli
37	96	100.0	352	14	US-10-439-845-2	Sequence 2, Appli
38	96	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
39	96	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
40	93	96.9	352	13	US-10-106-623-20	Sequence 20, Appli
41	82	85.4	22	14	US-10-239-423-43	Sequence 43, Appli
42	78	81.2	18	14	US-10-084-813-76	Sequence 76, Appli
43	78	81.2	32	14	US-10-057-890A-13	Sequence 13, Appli
44	78	81.2	32	14	US-10-072-301-9	Sequence 9, Appli
45	78	81.2	32	14	US-10-071-866-9	Sequence 9, Appli
46	78	81.2	32	14	US-10-239-423-42	Sequence 42, Appli
47	78	81.2	32	15	US-10-360-828-3	Sequence 3, Appli
48	78	81.2	32	15	US-10-360-828-9	Sequence 9, Appli
49	78	81.2	138	14	US-10-057-890A-10	Sequence 10, Appli
50	78	81.2	157	14	US-10-057-890A-31	Sequence 31, Appli
51	75	78.1	18	14	US-10-084-813-78	Sequence 78, Appli
52	74	77.1	21	14	US-10-225-567A-1492	Sequence 1492, Ap
53	74	77.1	27	15	US-09-805-375-4	Sequence 4, Appli
54	60	62.5	27	15	US-10-371-483-3	Sequence 3, Appli
55	47	49.0	18	14	US-10-084-813-79	Sequence 79, Appli
56	47	49.0	355	14	US-10-376-564-13	Sequence 13, Appli
57	45	46.9	355	14	US-10-164-649-53	Sequence 53, Appli
58	45	46.9	398	15	US-10-369-493-10241	Sequence 10241, A
59	44	45.8	332	14	US-10-095-876A-2	Sequence 2, Appli
60	44	45.8	616	14	US-10-260-877-120	Sequence 120, App
61	43	44.8	24	14	US-10-439-845-6	Sequence 6, Appli
62	43	44.8	25	9	US-09-864-761-38650	Sequence 38650, A
63	43	44.8	38	9	US-09-864-761-44083	Sequence 44083, A
64	43	44.8	233	9	US-09-731-872-306	Sequence 306, App
65	43	44.8	233	10	US-09-876-997-306	Sequence 306, App
66	43	44.8	237	10	US-09-769-744A-70	Sequence 70, Appli
67	43	44.8	275	9	US-09-925-300-1292	Sequence 1292, Ap
68	43	44.8	275	14	US-10-106-698-6216	Sequence 6216, Ap
69	43	44.8	344	9	US-09-912-025-2	Sequence 2, Appli
70	43	44.8	344	14	US-10-223-085-16	Sequence 16, Appli
71	43	44.8	344	14	US-10-223-084-16	Sequence 16, Appli
72	43	44.8	344	14	US-10-223-088-16	Sequence 16, Appli
73	43	44.8	344	14	US-10-223-090-16	Sequence 16, Appli
74	43	44.8	344	14	US-10-223-087-16	Sequence 16, Appli
75	43	44.8	344	14	US-10-225-567A-354	Sequence 354, App
76	43	44.8	344	14	US-10-223-083-16	Sequence 16, Appli
77	43	44.8	344	14	US-10-223-089-16	Sequence 16, Appli
78	43	44.8	344	14	US-10-095-876A-4	Sequence 4, Appli
79	43	44.8	344	14	US-10-223-081-16	Sequence 16, Appli
80	43	44.8	344	14	US-10-223-082-16	Sequence 16, Appli
81	43	44.8	348	14	US-10-029-386-32996	Sequence 32996, A
82	43	44.8	438	10	US-09-769-787-48	Sequence 48, Appli
83	43	44.8	957	16	US-10-389-566-1990	Sequence 1990, Ap
84	42	43.8	29	9	US-09-864-761-38300	Sequence 38300, A
85	42	43.8	460	13	US-10-033-078-4	Sequence 4, Appli
86	41	42.7	397	10	US-09-932-227-10	Sequence 10, Appli
87	41	42.7	397	14	US-10-183-708-10	Sequence 10, Appli
88	40	41.7	209	9	US-09-925-302-752	Sequence 752, App

Sequence 58, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 62, Appl
Sequence 2, Appli
Sequence 14, Appl
Sequence 62, Appl
Sequence 9, Appli
Sequence 2, Appli

89 40 41.7 279 15 US-10-174-364-58
90 40 41.7 355 9 US-09-961-068-1
91 40 41.7 355 9 US-09-961-068-1
92 40 41.7 355 9 US-09-938-719-9
93 40 41.7 355 9 US-09-938-719-9
94 40 41.7 355 9 US-09-938-719-9
95 40 41.7 355 14 US-10-225-567A-62
96 40 41.7 355 14 US-10-245-850-2
97 40 41.7 355 14 US-10-376-564-14
98 40 41.7 355 14 US-10-423-423-62
99 40 41.7 355 14 US-10-439-845-9
100 40 41.7 355 15 US-10-452-015-2

ALIGNMENTS

RESULT 1
US-10-084-813-13
; Sequence 13, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-13

Query Match 100.0%; Score 96; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
DB 1 SOYQFWKFNQTLKIVILG 18

RESULT 2
US-10-084-813-77
; Sequence 77, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

US-10-084-813-77

OTHER INFORMATION: Description of Artificial Sequence: binding peptide

US-10-084-813-77

Query Match 100.0%; Score 96; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
DB 1 SOYQFWKFNQTLKIVILG 18

RESULT 3
US-09-938-719-11
; Sequence 11, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-719-11

Query Match 100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVILG 18
DB 9 SOYQFWKFNQTLKIVILG 26

RESULT 4
US-09-939-226-11
; Sequence 11, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT

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; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-939-226-11
Query Match 100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKNFQTLKIVILG 18
DB 9 SOYQFWKNFQTLKIVILG 26
;
; RESULT 5
; US-09-938-703-11
; Sequence 11, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-703-11
Query Match 100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKNFQTLKIVILG 18
DB 9 SOYQFWKNFQTLKIVILG 26
;
; RESULT 6
; US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2
Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOYQFWKNFQTLKIVILG 18
DB 185 SOYQFWKNFQTLKIVILG 202
;
; RESULT 7
; US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Ferros, Mancosbos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC1034BPME
; CURRENT APPLICATION NUMBER: US/09/759,841
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; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 8
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 9
US-09-779-879A-2
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 10
US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 11
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258

; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 12

US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehit, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 13

US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehit, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 14

US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | | | | | |
DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 15

US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match 100.0%; Score 96; DB 9; Length 352;

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Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 16
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 17
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 18
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; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 18
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 18
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Db 185 SOYQFWKMFQTLKIVILG 202

RESULT 19

US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,703

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939

FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-938-703-5

Query Match 100.0%; Score 96; DB 9; Length 352;

Best Local Similarity 100.0%; Pred. No. 3.6e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKMFQTLKIVILG 18

Db 185 SOYQFWKMFQTLKIVILG 202

RESULT 20

US-09-502-783A-2

; Sequence 2, Application US/09502783A

; Patent No. US20020132269A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRE

; FILE REFERENCE: 1488.1150006

; CURRENT APPLICATION NUMBER: US/09/502,783A

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

Query Match 100.0%; Score 96; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 3.6e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SQYQFWKFNFTLKIVILG 18
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Db      185 SQYQFWKFNFTLKIVILG 202

RESULT 22
US-09-826-509-477
; Sequence 477, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 477
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-477

Query Match      100.0%; Score 96; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKFNFTLKIVILG 18
      |||||
Db      185 SQYQFWKFNFTLKIVILG 202

RESULT 23
US-10-106-623-2
; Sequence 23, Application US/10106623
; Publication No. US2002015088A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marehall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US2002015088A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match      100.0%; Score 96; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKFNFTLKIVILG 18
      |||||
Db      185 SQYQFWKFNFTLKIVILG 202

RESULT 24
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SQYQFWKFNFTLKIVILG 18
      |||||
Db      185 SQYQFWKFNFTLKIVILG 202

RESULT 25
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 26
US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 27
US-10-067-800-2
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 28
US-10-290-058A-6
; Sequence 6, Application US/10290038A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; FILE REFERENCE: MPI01-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-290-058A-6

Query Match      100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SQYQFWKNFQTLKIVILG 18
Db      185 SQYQFWKNFQTLKIVILG 202

RESULT 29
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenma C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352
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US-10-225-567A-352

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQWKNFQTLKIVILG 202

RESULT 30

US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/MAP/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-10-323-314-1

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQWKNFQTLKIVILG 202

Search completed: March 4, 2004, 18:22:52
Job time : 25.0612 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 52.3061 Seconds
(without alignments)
118.840 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIIVLLNTQEPFGNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	100.0	22	4	AAB88996
2	118	100.0	268	7	ADCI0142 Human NOV
3	118	100.0	268	7	ADCI0144 Human NOV
4	118	100.0	332	2	AAB26766 Human che
5	118	100.0	352	2	AAB27407 Human CCR
6	118	100.0	352	2	AAB27123 Human che
7	118	100.0	352	2	AAB27125 Human che
8	118	100.0	352	2	AAB27125 Macaque c
9	118	100.0	352	2	AAB27125 Human G-p
10	118	100.0	352	2	AAB27125 Human CC
11	118	100.0	352	3	AAB27125 HIV-1 co-
12	118	100.0	352	4	AAB27125 Human G-p
13	118	100.0	352	4	AAB27125 Amino aci
14	118	100.0	352	4	AAB27125 Human G-p
15	118	100.0	352	4	AAB27125 Human CCR
16	118	100.0	352	4	AAB27125 Human che
17	118	100.0	352	4	AAB27125 Human G-p
18	118	100.0	352	4	AAB27125 Human G-p
19	118	100.0	352	4	AAB27125 Human HDG
20	118	100.0	352	4	AAB27125 Human NOV
21	118	100.0	352	4	AAB27125 Human CCR
22	118	100.0	352	4	AAB27125 Human CCR
23	118	100.0	352	4	AAB27125 Human CCR
24	118	100.0	352	5	AAB27125 Human G-p
25	118	100.0	352	5	AAB27125 Human CCR

26	118	100.0	352	5	AAB27125 Human CC
27	118	100.0	352	5	AAB27125 Human G-p
28	118	100.0	352	5	AAB27125 Human imm
29	118	100.0	352	5	AAB27125 Human G-p
30	118	100.0	352	5	AAB27125 Human G-p
31	118	100.0	352	5	AAB27125 Human G-p
32	118	100.0	352	5	AAB27125 Human G-p
33	118	100.0	352	5	AAB27125 Human che
34	118	100.0	352	5	AAB27125 Human che
35	118	100.0	352	6	AAB27125 Human can
36	118	100.0	352	6	AAB27125 Human C-C
37	118	100.0	352	6	AAB27125 Human G-p
38	118	100.0	352	6	AAB27125 Amino aci
39	118	100.0	352	6	AAB27125 Human C-C
40	118	100.0	352	6	AAB27125 Human C-C
41	118	100.0	352	7	AAB27125 Human che
42	118	100.0	371	2	AAB27125 Macaque c
43	118	100.0	439	2	AAB27125 Human CC
44	108	91.5	354	2	AAB27125 Fusion pr
45	105	89.0	354	7	AAB27125 Mouse CC-
46	105	89.0	354	7	AAB27125 Rat Prote
47	103	87.3	329	4	AAB27125 Human MCP
48	103	87.3	329	5	AAB27125 Human MCP
49	103	87.3	344	5	AAB27125 Class I r
50	103	87.3	344	6	AAB27125 Human mon
51	103	87.3	360	2	AAB27125 Human mon
52	103	87.3	360	2	AAB27125 Human mon
53	103	87.3	360	4	AAB27125 Human CCR
54	103	87.3	360	4	AAB27125 Human CCR
55	103	87.3	360	4	AAB27125 Human will
56	103	87.3	360	4	AAB27125 Non-endog
57	103	87.3	360	6	AAB27125 Amino aci
58	103	87.3	360	6	AAB27125 Human C-C
59	103	87.3	374	2	AAB27125 Human mon
60	103	87.3	374	4	AAB27125 Human CCR
61	103	87.3	374	6	AAB27125 Human che
62	103	87.3	374	7	AAB27125 Human Pro
63	103	87.3	374	7	AAB27125 Human Pro
64	94	79.7	18	4	AAB27125 HIV gp120
65	93	78.8	18	4	AAB27125 HIV gp120
66	78	66.1	18	4	AAB27125 HIV gp120
67	74	62.7	20	4	AAB27125 CCR5 immu
68	71	60.2	18	4	AAB27125 HIV gp120
69	71	60.2	28	2	AAB27125 G-protein
70	70	59.3	344	2	AAB27125 Human che
71	70	59.3	344	2	AAB27125 Amino aci
72	70	59.3	344	5	AAB27125 Human PRO
73	70	59.3	344	5	AAB27125 Human G p
74	70	59.3	344	5	AAB27125 Human G p
75	70	59.3	344	6	AAB27125 Human ang
76	70	59.3	344	6	AAB27125 Human che
77	70	59.3	344	7	AAB27125 Human sec
78	70	59.3	344	7	AAB27125 Human sec
79	70	59.3	344	8	AAB27125 Human sec
80	70	59.3	344	8	AAB27125 Human mac
81	70	59.3	356	6	AAB27125 Human mon
82	70	59.3	356	6	AAB27125 Human mon
83	66	55.9	26	2	AAB27125 Peptide e
84	65	55.1	28	2	AAB27125 G-protein
85	63	53.4	15	7	AAB27125 CCR5 chem
86	61	51.7	25	2	AAB27125 CCR5 rece
87	61	51.7	25	2	AAB27125 CCR5 rece
88	57	48.3	16	2	AAB27125 Human CC
89	57	48.3	17	2	AAB27125 Synthetic
90	57	48.3	17	2	AAB27125 Peptide r
91	57	48.3	17	2	AAB27125 Alanine s
92	57	48.3	17	2	AAB27125 Alanine s
93	57	48.3	17	2	AAB27125 Alanine s
94	57	48.3	17	6	AAB27125 CC-chemok
95	57	48.3	17	6	AAB27125 Human CC-
96	57	48.3	18	4	AAB27125 HIV gp120
97	57	48.3	138	5	AAB27125 Human CCR
98	57	48.3	157	5	AAB27125 Human CCR

99 56 47.5 209 3 AAB58414 Lung canc
100 56 47.5 295 4 AAG80106 Human CCR

ALIGNMENTS

RESULT 1

AAB88996
ID AAB88996 standard; peptide; 22 AA.
XX
AC AAB88996;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #89.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX

PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.
XX
PS Claim 21; Page 38; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 118; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYIVLLINTFOFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 1 APYIVLLINTFOFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |

RESULT 2
ADCL0142
ID ADCL0142 standard; protein; 268 AA.
XX
AC ADCL0142;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human NOVX polypeptide SEQ ID NO: 162.
XX
KW cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
KW inflammatory disorder; chromosome mapping; tissue typing;

KW predictive medicine.
XX
OS Homo sapiens.
XX
PN WO2003000842-A2.
XX
PD 03-JAN-2003.
XX
PF 04-JUN-2002; 2002WO-US017443.
XX
PR 04-JUN-2001; 2001US-0295607P.
PR 04-JUN-2001; 2001US-0295661P.
PR 06-JUN-2001; 2001US-0296404P.
PR 06-JUN-2001; 2001US-0296418P.
PR 07-JUN-2001; 2001US-0296575P.
PR 11-JUN-2001; 2001US-0297414P.
PR 12-JUN-2001; 2001US-0295573P.
PR 12-JUN-2001; 2001US-0297567P.
PR 14-JUN-2001; 2001US-0298285P.
PR 15-JUN-2001; 2001US-0298528P.
PR 18-JUN-2001; 2001US-0299133P.
PR 19-JUN-2001; 2001US-0299230P.
PR 21-JUN-2001; 2001US-0299949P.
PR 22-JUN-2001; 2001US-0300177P.
PR 26-JUN-2001; 2001US-0300883P.
PR 28-JUN-2001; 2001US-0301530P.
PR 28-JUN-2001; 2001US-0301550P.
PR 03-JUL-2001; 2001US-0302951P.
PR 31-JUL-2001; 2001US-0308890P.
PR 14-SEP-2001; 2001US-0322297P.
PR 25-SEP-2001; 2001US-0324669P.
PR 03-DEC-2001; 2001US-0337477P.
PR 21-FEB-2002; 2002US-0341562P.
PR 21-FEB-2002; 2002US-0358656P.
PR 21-FEB-2002; 2002US-0359122P.
PR 22-FEB-2002; 2002US-0358978P.
PR 22-FEB-2002; 2002US-0359034P.
PR 22-FEB-2002; 2002US-0359035P.
PR 22-FEB-2002; 2002US-0359121P.
PR 27-FEB-2002; 2002US-0359964P.
PR 01-MAR-2002; 2002US-0360858P.
PR 12-MAR-2002; 2002US-0363430P.
PR 12-MAR-2002; 2002US-0363676P.
PR 10-APR-2002; 2002US-0371346P.
PR 10-MAY-2002; 2002US-0379444P.
PR 04-JUN-2002; 2002US-00379444.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Agee ML, Anderson DM, Berghs C, Casman SJ, Catterton E;
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalte T, Ji W, Kekuda R;
PI Khramsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet L;
PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
PI Rothenberg WE, Shenoy SG, Shinkels RA, Smithson G, Spaderna SK;
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX
WPI: 2003-210149/20.
DR N-PSDB; ADC10141.
XX

PT New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.

PS Claim 1; SEQ ID NO 162; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression

or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.

Sequence 268 AA;

Query Match 100.0%; Score 118; DB 7; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFOFFGLNCS 22
Db 165 APYIVILLNTFOFFGLNCS 186

RESULT 3
ADC10144
ID ADC10144 standard; protein; 268 AA.

AC ADC10144;

DT 18-DEC-2003 (first entry)

Human NOVX polypeptide SEQ ID NO: 164.

cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective; antiinflammatory; gene therapy; antisense therapy; thymimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.

Homo sapiens.

WO2003000842-A2.

03-JAN-2003.

04-JUN-2002; 2002WO-US017443.

04-JUN-2001; 2001US-0295607P.

06-JUN-2001; 2001US-0295661P.

06-JUN-2001; 2001US-0296404P.

06-JUN-2001; 2001US-0296418P.

07-JUN-2001; 2001US-0296575P.

11-JUN-2001; 2001US-0297414P.

12-JUN-2001; 2001US-0295573P.

12-JUN-2001; 2001US-0297567P.

14-JUN-2001; 2001US-0298285P.

15-JUN-2001; 2001US-0298528P.

18-JUN-2001; 2001US-0298133P.

13-JUN-2001; 2001US-0298230P.

21-JUN-2001; 2001US-0299949P.

22-JUN-2001; 2001US-0300177P.

26-JUN-2001; 2001US-0300883P.

28-JUN-2001; 2001US-0301530P.

28-JUN-2001; 2001US-0301550P.

03-JUL-2001; 2001US-0302951P.

31-JUL-2001; 2001US-0308890P.

12-MAR-2002; 2002US-0363676P.
10-APR-2002; 2002US-0371346P.
10-MAY-2002; 2002US-0379444P.
04-JUN-2002; 2002US-0379444.

(CURA-) CURAGEN CORP.

Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
Rotherberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
Spytek JA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
Burgess CE, Lepley DM;

WPI; 2003-210149/20.
N-ESDE; ADC10143.

New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.

Claim 1; SEQ ID NO 164; 772pp; English.

The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression or activity of the polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to one of the polypeptides of the invention.

Sequence 268 AA;

Query Match 100.0%; Score 118; DB 7; Length 268;

Best Local Similarity 100.0%; Pred. No. 2.1e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFOFFGLNCS 22

Db 165 APYIVILLNTFOFFGLNCS 186

RESULT 4

AAW26766

ID AAW26766 standard; protein; 332 AA.

AC AAW26766;

DT 21-MAY-1998 (first entry)

Human chemokine receptor MMLR-CCR.

Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human; monocyte; macrophage; chemotaxis; haematopoiesis; infection; inflammation; proliferative disease; cardiovascular disease; tumour; rheumatoid arthritis; alveolitis; atherosclerosis; chronic granulomatous disease; asthma; myasthenia gravis; diabetes; inflammatory bowel disease; toxic shock syndrome; septic shock; Chediak-Higashi syndrome; therapy; diagnosis.

Homo sapiens.

Key Location/Qualifiers

Peptide 107..128

/note= "conserved peptide"

Misc-difference 121

/note= "a claimed polypeptide has isoleucine at residue

FT XX 121"

PN WO9741225-A2.

XX 06-NOV-1997.

PD 25-APR-1997; 97WO-US006993.

XX 26-APR-1996; 96US-00638081.

XX (INCY-) INCYTE PHARM INC.

PA Au-Young J, Bandman O, Coleman R, Wilde CG;

XX WPI; 1997-549729/50.

XX N-PSDB; AAT99542.

XX Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease.

XX Claim 8; Page 37-38; 59pp; English.

XX This protein comprises human MMLR-CCR, a novel C-C chemokine receptor associated with monocyte/macrophage infiltration and chemotaxis and haematopoiesis. The amino acid sequence was deduced from a cDNA clone (see AAT99542) obtained from a cDNA library made from mononuclear cells collected on day 2 of a mixed lymphocyte culture, i.e. cells associated with inflammation and immunomodulation. Another novel chemokine receptor, MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7 transmembrane spanning segments connected by a series of intracellular and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study, diagnose and treat disease states in which normal leukocyte function is perturbed by normal leukopoiesis or inappropriate activation via chemokine agonists or antagonists, such as infection, inflammation, CC proliferative disease, tumorigenesis, autoimmune disease, abnormal cell proliferation, solid tumours, cardiovascular disease, rheumatoid arthritis, alveolitis, atherosclerosis, chronic granulomatous disease, asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic shock syndrome, septic shock and Chediak-Higashi syndrome

XX SQ Sequence 332 AA;

Query Match 100.0%; Score 118; DB 2; Length 332;

Best Local Similarity 100.0%; Pred. No. 2.7e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFQFFGLNCS 22

DB 229 APYNVILLNTFQFFGLNCS 250

RESULT 5

AAW27407

ID AAW27407 standard; protein; 352 AA.

XX AAW27407;

XX 14-APR-1998 (first entry)

XX Human CCR5.

XX Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;

XX inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;

XX idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;

XX atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX WO9732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-BE000023.

XX 01-MAR-1996; 96EP-00870021.

XX 06-AUG-1996; 96EP-00870102.

XX (EURO-) EUROSREEN SA.

XX Samson M, Parmentier M, Vassart G, Libert P;

XX WPI; 1997-479829/44.

XX N-PSDB; AAT90117.

XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.

XX Claim 4; Fig 1b-c; 94pp; English.

XX The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFQFFGLNCS 22

DB 249 APYNVILLNTFQFFGLNCS 270

RESULT 6

AAW27123

ID AAW27123 standard; protein; 352 AA.

XX AAW27123;

XX 14-DEC-1997 (first entry)

XX Human chemokine receptor 88C.

XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..32

FT /label= Extracellular_domain

FT Domain 56..67

FT /label= Intracellular_domain

FT Domain 89..112

FT /label= Extracellular_domain

FT Domain 125..145

FT /label= Intracellular_domain

FT Domain 166..191

FT /label= Extracellular_domain

FT Domain 213..235

FT /label= Intracellular_domain

FT Domain 259..280

FT /label= Extracellular_domain

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FT Domain 301..352
XX /label= Intracellular_domain
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX N-PSDB; AAT85161.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 16; Page 47-48; 65pp; English.
XX
XX This polypeptide sequence comprises novel human chemokine receptor 88C, a
XX G protein coupled receptor that is involved in leukocyte trafficking. Its
XX amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
XX macrophage library. It shows 62% identity to CCKXR1. Chemokine receptor
XX 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
XX and their polypeptide fragments can be produced in transformed host
XX cells. The receptors, peptides comprising one or more of the
XX extracellular or intracellular domains, and anti-receptor antibodies can
XX be used to modulate receptor activities, particularly ligand and G
XX protein binding, and are potentially useful in the treatment
XX of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX infection, AIDS, inflammatory conditions, pathological immune response,
XX abnormal haematopoietic processes etc
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 APYNIVLLNTFOEFFGLNCS 22
XX |||||
XX DB 249 APYNIVLLNTFOEFFGLNCS 270
XX
XX RESULT 7
XX AAW27125
XX ID AAW27125 standard; protein; 352 AA.
XX
XX AC AAW27125;
XX
XX 14-DEC-1997 (first entry)
XX
XX Macaque chemokine receptor 88C.
XX
XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX modulator; antibody.
XX
XX Macaca sp.
XX
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX Human G-protein chemokine receptor, HDGMR10 - useful to identify

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PR 20-DEC-1995; 95US-00575967.
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX N-PSDB; AAT85161.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 36; Page 57-58; 65pp; English.
XX
XX This polypeptide sequence comprises macaque chemokine receptor 88C, a
XX G protein coupled receptor that is involved in leukocyte trafficking. Its
XX amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX amplification. It shows 97% identity to human 88C (AAW27123). 88C
XX receptors and their polypeptide fragments can be produced in transformed
XX host cells. The receptors, peptides comprising one or more of the
XX extracellular or intracellular domains, and anti-receptor antibodies can
XX be used to modulate receptor activities, particularly ligand and G
XX protein binding, and are potentially useful in the treatment
XX of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX infection, AIDS, inflammatory conditions, pathological immune response,
XX abnormal haematopoietic processes etc. A hybridoma that produces an
XX antibody that specifically binds to macaque 88C is claimed
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 APYNIVLLNTFOEFFGLNCS 22
XX |||||
XX DB 249 APYNIVLLNTFOEFFGLNCS 270
XX
XX RESULT 8
XX AAW07602
XX ID AAW07602 standard; protein; 352 AA.
XX
XX AC AAW07602;
XX
XX 26-FEB-1997 (first entry)
XX
XX Human G-protein chemokine receptor HDGMR10.
XX
XX G-protein chemokine receptor; HDGMR10; signal transduction;
XX haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
XX therapy.
XX
XX Homo sapiens.
XX
XX WO9639437-A1.
XX
XX 12-DEC-1996.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 1997-043072/04.
XX N-PSDB; AAT44042.
XX
XX Human G-protein chemokine receptor, HDGMR10 - useful to identify

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PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
 PT acute inflammation, rheumatoid arthritis, etc.
 XX
 PS Claim 1; Page 44-46; 61pp; English.
 XX
 CC Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7
 CC -transmembrane protein involved in signal transduction. Its amino acid
 CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human
 CC monocyte library. Isolation of the cDNA allows prodn. of recombinant
 CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
 CC receptor can be used to identify agonists or antagonists of the receptor;
 CC such cDns. can be used to treat conditions related to the under- and over
 CC -expression of G-protein chemokine receptors
 XX
 XX Sequence 352 AA;
 XX
 XX Query Match 100.0%; Score 118; DB 2; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYIVILLNTFQFFGLNCS 22
 Db 249 APYIVILLNTFQFFGLNCS 270
 RESULT 9
 AAW23835
 ID AAW23835 standard; protein; 352 AA.
 XX
 AC AAW23835;
 XX
 XX 08-JUN-1998 (first entry)
 DT Human CC chemokine receptor 5 (CCR5).
 DE
 DE Human CC chemokine receptor 5 (CCR5).
 XX
 CC chemokine receptor 5; CCR5; G-protein coupled receptor;
 KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Domain 29..55
 FT /label= I
 FT /note= "transmembrane domain"
 FT Domain 104..126
 FT /label= III
 FT /note= "transmembrane domain"
 FT Region 109..120
 FT /note= "extracellular loop-1 (Claim 19)"
 FT Domain 143..171
 FT /label= IV
 FT /note= "transmembrane domain"
 FT Region 187..210
 FT /note= "extracellular loop-2 (Claim 19)"
 FT Domain 194..219
 FT /label= V
 FT /note= "transmembrane domain"
 FT Domain 238..258
 FT /label= VI
 FT /note= "transmembrane domain"
 FT Region 261..276
 FT /note= "extracellular loop-3 (Claim 19)"
 FT Domain 277..300
 FT /label= VII
 FT /note= "transmembrane domain"
 XX
 PN WO9745543-A2.
 XX
 PD 04-DEC-1997.
 XX
 XX 28-MAY-1997; 97WO-US009586.
 XX
 XX 28-MAY-1996; 96US-0018508P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
 PI Broder CC, Kennedy PE;
 XX
 DR WPI; 1998-032650/03.
 DR N-PSDB; AAT76920.
 XX
 PT CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 PT between HIV and a target cell.
 XX
 PS Claim 68; Fig 1C; 70pp; English.
 XX
 XX This protein sequence comprises of a novel human macrophage-selective CC
 CC chemokine receptor that has been designated CCR5. The sequence was
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27leu variant
 CC (see W238340 of CCR5 was also identified. The susceptibility of human
 CC macrophages to HIV infection depends on cell surface expression of CD4
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
 CC protein coupled cell surface molecules. It plays an essential role in the
 CC membrane fusion step of infection by some HIV isolates. The establishment
 CC of stable, non-human cell lines and transgenic mammals having cells that
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 CC agents capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV
 XX
 SQ Sequence 352 AA;
 XX
 XX Query Match 100.0%; Score 118; DB 2; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYIVILLNTFQFFGLNCS 22
 Db 249 APYIVILLNTFQFFGLNCS 270
 RESULT 10
 AAW88232
 ID AAW88232 standard; protein; 352 AA.
 XX
 AC AAW88232;
 XX
 DT 15-MAR-1999 (first entry)
 DT HIV-1 co-receptor CCR5.
 DE
 DE HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 KW gene therapy; human.
 KW
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Domain 32..56
 FT /note= "transmembrane domain 1"
 FT Domain 67..87
 FT /note= "transmembrane domain 2"
 FT Misc-difference 101
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 FT (Stop) in CCR5m303"
 FT Domain 103..124
 FT /note= "transmembrane domain 3"
 FT Domain 142..167
 FT /note= "transmembrane domain 4"
 FT Domain 200..223
 FT /note= "transmembrane domain 5"
 FT Domain 236..260
 FT /note= "transmembrane domain 6"
 FT Domain 275..301
 FT /note= "transmembrane domain 7"
 FT

XX WO9854317-A1.
 XX 03-DEC-1998.
 XX 29-MAY-1998; 98WO-EP003437.
 XX 30-MAY-1997; 97US-0048057P.
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
 XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
 XX WPI; 1999-059835/05.
 XX N-PSDB; AAV84126.
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 XX resistance of CCR5-expressing cells to HIV-1 infection.
 XX Disclosure; Page 34-35; 55pp; English.
 XX This is the amino acid sequence of wild-type human CCR5, which serves as
 XX a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 XX HIV-1. The invention relates to the identification of a CCR5 variant (see
 XX AAV88231), designated CCR5m303, comprising the first two transmembrane
 XX domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 XX presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 XX positive correlation with resistance to infection with M-tropic HIV-1
 XX strains, and may indicate slower progression of the disease. The
 XX detection of CCR5 variants may be used to identify individuals at lower
 XX risk of infection relative to the general population who, if infected,
 XX may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
 XX 36) are provided for use in diagnostic methods for detecting the presence
 XX of such variants. A method is provided for inhibiting HIV-1 infection of
 XX a cell expressing the CCR5 receptor. This involves introducing a nucleic
 XX acid encoding a CCR5 variant into the cell, thereby reducing the number
 XX of functional CCR5 molecules present on the cell surface

XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
 |||||
 Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 11
 AAY80128
 ID AAY80128 standard; protein; 352 AA.
 AC AAY80128;
 XX 19-MAY-2000 (first entry)
 XX Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.
 XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 XX diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 XX tumour; infection; leukaemia; psoriasis; allergy;
 XX T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;
 XX inflammation; allergic reaction; silicosis; sarcoidosis;
 XX rheumatoid arthritis; hyper-eosinophilia syndrome.
 XX Homo sapiens.
 XX US6025154-A.
 XX 15-FEB-2000.
 XX 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Li Y, Ruben SM;
 XX WPI; 2000-181807/16.
 XX N-PSDB; AAZ91481.
 XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 XX for diagnostic assays, scientific research and screening for compounds
 XX which bind to and activate or inhibit activation of the receptor
 XX polypeptides.
 XX Claim 1; Fig 1; 22pp; English.
 XX The present sequence represents a human G-protein chemokine receptor
 XX designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 XX screening for compounds which bind to and either: (1) activate the
 XX HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 XX healing, coagulation, and angiogenesis; treatment of solid tumours,
 XX chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 XX parasitic infections, psoriasis, and to stimulate growth factor activity;
 XX or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 XX preventing and/or treating allergy, atherogenesis, anaphylaxis,
 XX E-mediated allergic reactions, prostaglandin-independent fever, bone
 XX marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 XX hyper-eosinophilia syndrome. The polynucleotides are also useful for
 XX diagnostic assays for detecting diseases related to mutations in the
 XX nucleic acid sequences encoding the polypeptides and for detecting an
 XX altered level of the soluble form of the receptor polypeptides. The
 XX polynucleotides are also useful for in vitro purposes related to
 XX scientific research, synthesis of DNA and manufacture of DNA vectors

XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
 |||||
 Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 12
 AAG79089
 ID AAG79089 standard; protein; 352 AA.
 AC AAG79089;
 XX 10-DEC-2001 (first entry)
 XX Amino acid sequence of human CCR5 protein.
 XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 XX C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX Homo sapiens.
 XX WO200164752-A2.
 XX 07-SEP-2001.
 XX 28-FEB-2001; 2001WO-US006322.
 XX 02-MAR-2000; 2000US-00517605.
 XX (UYN)) UNIV NEW YORK STATE.
 XX (UTNI-) UNIV NIJMEGEN.

PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX WPI; 2001-602565/68.
 XX
 PT An antibody for the treatment or prevention of HIV-infection comprises a
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 FT DC-SIGN due to concomitant conformational change.
 XX
 XX
 PS Disclosure; Page 118-119; 131pp; English.
 XX
 CC The specification describes an antibody which is specific for an
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant
 CC conformational change. DC-SIGN is a receptor that is specifically
 CC expressed on dendritic cells and facilitates infection of T lymphocytes
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 CC with high affinity. The antibody of the invention inhibits the trans
 CC enhancement of HIV entry into a T cell or macrophage facilitated by
 CC dendritic cells. The antibody is useful to treat or prevent HIV
 CC infection. The present sequence represents a human CCR5 protein, which is
 CC a translocation promoting agent that interacts with CD4. This receptor
 CC functions in HIV-1 entry into cells
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVILLNTFQEFFGLNCS 22
 DB 249 APYIVILLNTFQEFFGLNCS 270
 |||||
 |||||

RESULT 13
 ARE07046
 ID AAE07046 standard; protein; 352 AA.
 XX
 AC AAE07046;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytosatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FT Domain 1..36
 FT /label= Extracellular_domain
 FT 37..305
 FT /label= Transmembrane_domain
 FT 37..58
 FT /label= Transmembrane_domain
 FT /note= "Segment 1"
 FT 59..67
 FT /label= Intracellular_loop_1
 FT 68..88
 FT /label= Transmembrane_domain
 FT /note= "Segment 2"
 FT 89..102
 FT /label= Extracellular_loop_1
 FT 103..124

FT /label= Transmembrane_domain
 FT 125..141
 FT /note= "Segment 3"
 FT /label= Intracellular_loop_2
 FT 142..166
 FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT 167..195
 FT /label= Extracellular_loop_2
 FT 196..223
 FT /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT 224..235
 FT /label= Intracellular_loop_3
 FT 236..260
 FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT 261..274
 FT /label= Extracellular_loop_3
 FT 287..305
 FT /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT 306..352
 FT /label= Intracellular_domain
 FT XX
 PN WO200158916-A2.
 XX
 XX 16-AUG-2001.
 PD
 XX
 PF 09-FEB-2001; 2001WO-US004153.
 XX
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 FI
 XX WPI; 2001-488966/53.
 DR N-PSDB; AAD13282.
 DR
 XX
 XX
 PS Claim 102; Fig 1; 518pp; English.
 XX
 CC The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGNR10 protein
 XX

SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFQEFGLNCS 22
|||||

DB 249 APYNVILLNTFQEFGLNCS 270

RESULT 14

AAE07048
ID AAE07048 standard; protein; 352 AA.

XX AAE07048;

DT 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerability;
 KW cytosolic; immunosuppressive; neutrotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HOMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX N-PSDB; AAD13299.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the

CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGNR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 1 APYNVILLNTFQEFGLNCS 22
|||||

DB 249 APYNVILLNTFQEFGLNCS 270

RESULT 15

AAG80111
ID AAG80111 standard; protein; 352 AA.

XX AAG80111;

XX 17-JAN-2002 (first entry)

XX Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.

XX Homo sapiens.

XX WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPEP-) IPF PHARM GMEH.

XX (FORS/) FORSMANN U.

XX Forssmann W, Adermann K, Heitland A, Spodsborg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.

XX Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antirheumatic, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine

CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQEPFFGLNCS 22

DB 249 APYNVILLNTQEPFFGLNCS 270

RESULT 16

AAE04321

ID AAE04321 standard; protein; 352 AA.

XX AAE04321;

DT 04-SEP-2001 (first entry)

DB Human chemokine receptor (CCR), CC-CR-5 related protein #2.

KW Human; transformed mammalian cell; CD4; reporter gene; translocation;

KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;

KW Chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;

KW CC-CR-5; envelope glycoprotein; anti-HIV.

XX Homo sapiens.

OS US6258527-B1.

PN 10-JUL-2001.

PD 21-MAY-1997; 97US-00861105.

PF 20-MAY-1996; 96US-0017157P.

PR 19-JUN-1996; 96US-0030043P.

PR 19-MAY-1997; 97US-00858660.

XX (AARO-) AARON DIAMOND AIDS RES CENT.

PA (UUNY) UNIV NEW YORK STATE.

PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

DR N-PSDB; RAD08577.

XX Transformed mammalian cell (T) that contains a CD4 gene, reporter gene

PT and HIV LTR for identification of drugs and antibodies for treatment of

PT HIV.

XX Disclosure; Col 47-50; 37pp; English.

PS The present invention relates to a transformed mammalian cell that

XX contains a gene encoding CD4, a construct encoding a reporter gene under

CC the regulation of an human immuno deficiency virus (HIV) long terminal

CC repeat (LTR) and that has been transduced with a vector encoding a human

CC chemokine receptor (CCR) where the CD4 and the CCR are present on the

CC cell surface of transformed mammalian cell. The invention is useful for

CC identifying drugs or antibodies that interfere with the translocation of

CC HIV into transformed mammalian cell or for identifying a human chemokine

CC receptor that facilitates the infection of a particular HIV strain into

CC the transformed mammalian cell. Compounds identified can be used to treat

CC cellular dysfunction and to prevent or combat HIV infection. The present

CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.

CC CC-CR-5 is the principal cofactor for entry mediated by the envelope

CC glycoproteins of primary macrophage-tropic strains of HIV-1

XX Sequence 352 AA;

SQ Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQEPFFGLNCS 22

DB 249 APYNVILLNTQEPFFGLNCS 270

RESULT 17

AAE07037

ID AAE07037 standard; protein; 352 AA.

XX AAE07037;

DT 16-OCT-2001 (first entry)

DB Human G-protein chemokine receptor (CCRS) HDGMR10 protein #1.

KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;

KW human immunodeficiency virus; antimicrobial; vasodilator; vulnherary;

KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;

KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;

KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;

KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;

KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;

KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;

KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

OS Key

XX Location/Qualifiers

FT 1..36 /label= Extracellular_domain

FT 37..305 /label= Transmembrane_domain

FT 37..58 /label= Transmembrane_domain

FT 59..67 /note= "Segment 1"

FT 68..88 /label= Intracellular_loop_1

FT 89..102 /label= Transmembrane_domain

FT 103..124 /note= "Segment 2"

FT 125..141 /label= Extracellular_loop_1

FT 142..166 /label= Transmembrane_domain

FT 167..195 /note= "Segment 3"

FT 196..223 /label= Intracellular_loop_2

FT 224..235 /label= Transmembrane_domain

FT 236..260 /note= "Segment 4"

FT 261..274 /label= Extracellular_loop_2

FT 287..305 /label= Transmembrane_domain

FT 306..352 /note= "Segment 5"

FT /label= Intracellular_loop_3

FT /label= Transmembrane_domain

FT /label= "Segment 6"

FT /label= "Segment 7"

FT /label= Intracellular_domain

XX WO200158915-A2.

PN 16-AUG-2001.

PD

XX 09-FEB-2001; 2001WO-US004152.
 XX
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 XX N-PSDB; AAD13181.
 DR
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX
 XX Claim 102; Fig 1; 495pp; English.
 PS
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound
 CC healing
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
 DB 249 APYNIVLLNTFQFFGLNCS 270
 RESULT 18
 AAEE07039
 ID AAEE07039 standard; protein; 352 AA.
 XX
 AC AAEE07039;
 XX
 XX 16-OCT-2001 (first entry)
 DT
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
 DE
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytosatic; immunosuppressive; nootropic; neuroprotective; Gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;

KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 OS Homo sapiens.
 XX WO200158915-A2.
 XX
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004152.
 PF
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 XX N-PSDB; AAD13198.
 DR
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX
 XX Example 40; Page 486-487; 495pp; English.
 PS
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation,
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 CC a neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 CC disorders (myocardial ischaemias) and wound healing
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
 DB 249 APYNIVLLNTFQFFGLNCS 270
 RESULT 19
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX
 AC AAB46858;
 XX
 XX 16-AUG-2001 (revised)
 DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 XX

DE XX Human HDGMR10 protein.

KW HDGMR10; human; G-protein chemokine receptor; antiinflammatory;
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
 KW cytostatic; antiparasitic; antipsoiatic; antirheumatic; antiarthritic;
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
 KW hyper-eosinophilic syndrome; vulnery.

XX OS Homo sapiens.

XX PN US200100241-A1.

XX PD 12-APR-2001.

XX PF 29-NOV-2000; 2000US-00725285.

XX PR 06-JUN-1995; 95US-00466343.

XX PR 18-NOV-1998; 98US-00195662.

XX PR 25-JUN-1999; 99US-00339912.

XX PA (LIYY// LI Y.

XX PA (RUBE//) RUBEN S M.

XX PI Li Y, Ruben SM;

XX PT WPI; 2001-226317/23.

XX DR N-PSDB; AAF26390.

XX PS New human G-protein chemokine receptor polypeptides and polynucleotides,
 PT useful for identifying (ant)agonists to the G-protein chemokine receptor.

XX PS Claim 1a; Page 15; 22pp; English.

XX CC This invention describes a novel receptor polypeptide (I) selected from
 CC (i) a fully defined 329 amino acid sequence (ii) fully disclosed in the
 CC specification; and (iii) a polypeptide encoded by the cDNA contained in a
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
 CC products of the invention have antiinflammatory, immunomodulatory,
 CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,
 CC antiparasitic, antipsoiatic, antirheumatic, antiarthritic and vasotropic
 CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors HDGMR10, (I) are useful for screening for compounds which
 CC activate or inhibit activation of (I). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 CC stimulating growth factor activity. HDGMR10 is useful for treating
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYIVILLNTTQEFFGLNCS 22
 |||||

Db 249 APYIVILLNTTQEFFGLNCS 270
 |||||

RESULT 20
 ABB56342

ID ABB56342 standard; protein; 352 AA.

XX ABB56342;

XX AC 18-FEB-2002 (first entry)

XX DT Non-endogenous human GPCR protein, SEQ ID NO: 477.

XX DE Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 XX constitutively activated GPCR; agonist; disease.

XX KW Homo sapiens.

XX OS Synthetic.

XX PN W0200177172-A2.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US011098.

XX PR 07-APR-2000; 2000US-0195747P.

XX PA (AREX-) ARENA PHARM INC.

XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;

XX DR WPI; 2001-648759/74.

XX DR N-PSDB; ABI97978.

XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.

XX PS Claim 1; Page 277-278; 394pp; English.

XX CC The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYIVILLNTTQEFFGLNCS 22
 |||||

Db 249 APYIVILLNTTQEFFGLNCS 270
 |||||

RESULT 21
 ABB563354

ID ABB563354 standard; protein; 352 AA.

XX AC AAB83354;

XX DT 09-OCT-2001 (first entry)

XX DE Human CCR5 protein sequence.

XX KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 XX human immunodeficiency virus; anti-inflammatory disease; human.

XX OS Homo sapiens.

XX PN EP1118858-A2.

XX PD 25-JUL-2001.

XX PF 03-JAN-2001; 2001EP-00300020.

XX 12-JAN-2000; 2000GB-00000659.
 PR 12-JAN-2000; 2000GB-00000661.
 PR 12-JAN-2000; 2000GB-00000663.
 XX (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX Dobbs S, Perros M, Rickett GA;
 PI WPI; 2001-477088/52.
 XX N-PSDB; AAF87099.
 DR
 XX
 PT Determining if an agent can modulate CCR5-gp120 interaction, comprises
 PT incubating the agent with CCR5 and gp120 and determining if the agent
 PT modulates the interaction.
 XX
 PS Claim 1; Page 110; 113pp; English.
 XX
 CC This sequence represents the human CCR5 protein sequence. The invention
 CC relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNTVLLNTFOEFGGLNCS 22
 DB 249 APYNTVLLNTFOEFGGLNCS 270
 RESULT 22
 AAB82948
 ID AAB82948 standard; protein; 352 AA.
 AC AAB82948;
 XX
 DT 21-DEC-2001 (first entry)
 DE Human HIV-1 co-receptor CCR5.
 XX
 KW CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 KW infection; therapy; vaccine; anti-HIV-1.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 2..18
 FT /note= "binds to HIV-1 gp120"
 XX
 PN WC200164710-A2.
 XX
 PD 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006699.
 PF
 XX 29-FEB-2000; 2000US-0185667P.
 PR
 PR 19-MAY-2000; 2000US-0205839P.
 PR

PR 07-FEB-2001; 2001US-0267231P.
 XX (PROG-) PROGENICS PHARM INC.
 PA (AARO-) AARON DIAMOND AIDS RES CENT.
 XX
 PI Dragic T, Olson WC;
 DR WPI; 2001-611273/70.
 DR N-PSDB; AAH26903.
 XX
 PT Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
 PT receptor) amino terminal domain including negatively charged and two
 PT sulfated tyrosine residues is useful for treating HIV infection in
 PT humans.
 XX
 PS Claim 1; Page 30; 163pp; English.
 XX
 CC The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
 CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
 CC site that determines the specificity of the interaction between CCR5 and
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
 CC CCR5 N-terminus is required for gp120 binding and may critically modulate
 CC the susceptibility of target cells to HIV-1 infection in vivo. The
 CC invention provides claimed sulfated peptides (see AAB82947) that are
 CC based on the CCR5 N-terminal region and which are effective for
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
 CC cells from becoming infected with HIV, of treating a subject whose CD4+
 CC cells are infected with HIV, and of identifying an agent which inhibits
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
 CC out in a subject, especially a human, infected (therapeutic method), not
 CC infected with HIV (prophylactic method), or in a subject who is not
 CC infected with, but has been exposed to, HIV
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNTVLLNTFOEFGGLNCS 22
 DB 249 APYNTVLLNTFOEFGGLNCS 270
 RESULT 23
 AAU97150
 ID AAU97150 standard; protein; 352 AA.
 AC AAU97150;
 XX
 DT 13-AUG-2002 (first entry)
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002048786-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 09-FEB-2001; 2001US-00779879.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 PR
 PA (ROSE/) ROSEN C A.

22-SEP-2000; 2000US-0234336P.

WO200171346-A2

XX

PD 27-SEP-2001.
 XX 21-MAR-2001; 2001WO-US009155.
 XX 21-MAR-2000; 2000US-0190946P.
 PR 21-MAR-2000; 2000US-0190946P.
 PR 21-MAR-2000; 2000US-0190996P.
 PR 21-MAR-2000; 2000US-0191299P.
 PR 20-MAR-2001; 2001US-00813448.
 PR 20-MAR-2001; 2001US-00813651.
 PR 20-MAR-2001; 2001US-00813653.
 XX (CONS-) CONSENSUS PHARM INC.
 PA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
 XX WPI; 2002-010610/01.
 XX N-PSDB; ABA02318.
 DR Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 XX comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.
 XX Example 3; Fig 4B; 50pp; English.
 PS The invention relates to a method for identifying a binding compound for
 XX CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention,
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided methods for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents a naturally occurring variant of human CCR5 in which
 CC there is a glutamine, rather than a leucine, at position 55
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFQFFGLNCS 22
 DB 249 APYNIVLLNTFQFFGLNCS 270
 RESULT 26
 ID AAM52828 standard; protein; 352 AA.
 XX AC AAM52828;
 XX DT 22-FEB-2002 (first entry)
 XX Human CC chemokine receptor 5 (CCR5).
 DE CCR5; CC chemokine receptor 5; human; HIV infection;
 XX human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification.
 XX Homo sapiens.
 OS WC200171346-A2.
 PN 27-SEP-2001.
 PD 27-SEP-2001.
 XX

PF 21-MAR-2001; 2001WO-US009155.
 XX 21-MAR-2000; 2000US-0190946P.
 PR 21-MAR-2000; 2000US-0190996P.
 PR 21-MAR-2000; 2000US-0191299P.
 PR 20-MAR-2001; 2001US-00813448.
 PR 20-MAR-2001; 2001US-00813651.
 PR 20-MAR-2001; 2001US-00813653.
 XX (CONS-) CONSENSUS PHARM INC.
 PA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
 XX WPI; 2002-010610/01.
 XX N-PSDB; ABA02317.
 DR Identifying CC chemokine receptor 5 binding compound for treating AIDS,
 XX comprises binding a molecule from library to a molecule having binding
 PT property corresponding to CCR5 and identifying bound molecule.
 XX Example 3; Fig 4A; 50pp; English.
 PS The invention relates to a method for identifying a binding compound for
 XX CC chemokine receptor 5 (CCR5). The method involves screening a library
 CC of test molecules (particularly peptides) with immobilised CCR5, and then
 CC identifying those molecules which bind. The invention also relates to
 CC CCR5-binding molecules identified using the method of the invention,
 CC methods for identifying consensus motifs for CCR5-binding peptides, a
 CC transfer vector encoding tagged CCR5, a computer-aided methods for
 CC determining the relative binding affinity of a test molecule to CCR5 and
 CC a computer aided drug screening assay that utilises the three-dimensional
 CC structure of CCR5. Compounds identified using the methods of the
 CC invention are useful for treating or preventing HIV (human
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
 CC syndrome) in a patient. The methods of the invention may also be used to
 CC identify agonists or antagonists of the interaction of CCR5 with its
 CC natural ligand, and to determine a binding motif for CCR5. The present
 CC sequence represents human CCR5
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNIVLLNTFQFFGLNCS 22
 DB 249 APYNIVLLNTFQFFGLNCS 270
 RESULT 27
 ID ABG70597 standard; protein; 352 AA.
 XX AC ABG70597;
 XX DT 03-DEC-2002 (first entry)
 XX Human G-protein chemokine receptor, HDGNR10.
 DE Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;
 XX haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;
 KW chronic infection; leukaemia; T-cell mediated autoimmune disease;
 KW parasitic infection; psoriasis; growth factor activity; allergy;
 KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;
 KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;
 KW prostaglandin-independent fever; bone marrow failure; shock;
 KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;
 KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;
 KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;
 KW antipyretic; receptor.
 XX Homo sapiens.
 OS

XX US2002099176-A1.
 XX 25-JUL-2002.
 XX 25-JUN-1999; 99US-00339912.
 XX 06-JUN-1995; 95US-00466343.
 XX (LIYY/) LI Y.
 XX (RUBEN/) RUBEN S M.
 XX Li Y, Ruben SM;
 XX WPI; 2002-690494/74.
 XX N-PSDB; ABS54272.
 XX Novel human G-protein chemokine receptor polypeptide useful for
 PT identifying modulators for stimulating hematopoiesis, wound healing,
 PT leukemia, for treating allergy, rheumatoid arthritis, shock and as
 PT research agents.
 XX Claim 7; Fig 1; 22pp; English.
 XX The present invention relates to the isolation of human G-protein
 CC chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide
 CC sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences
 CC are useful for diagnosing a disease or a susceptibility to a disease
 CC related to underexpression of HDGNR10. They are useful for identifying
 CC modulators for stimulating hematopoiesis, wound healing, coagulation,
 CC angiogenesis, to treat solid tumors, chronic infections, leukaemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or
 CC for stimulating growth factor activity. The sequences are also useful for
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,
 CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be
 CC used in gene therapy to treat conditions related to underexpression of
 CC HDGNR10. The present sequence represents human G-protein chemokine
 CC receptor, HDGNR10
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYIVILLNTQEFGLNCS 22
 DB 249 APYIVILLNTQEFGLNCS 270
 RESULT 28
 ABG92883
 ID ABG92883 standard; protein; 352 AA.
 XX ABG92883;
 XX 19-NOV-2002 (first entry)
 XX Human immunoglobulin variable heavy domain #1.
 XX Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.

XX Homo sapiens.
 XX OS
 XX WO200264612-A2.
 XX 22-AUG-2002.
 XX 08-FEB-2002; 2002WO-US003634.
 XX 09-FEB-2001; 2001US-00779880.
 XX 09-FEB-2001; 2001WO-US004153.
 XX 12-JUN-2001; 2001US-0297257P.
 XX 08-AUG-2001; 2001US-0310458P.
 XX 12-OCT-2001; 2001US-0328447P.
 XX 21-DEC-2001; 2001US-0341725P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Roschke V, Rosen CA, Ruben SM;
 XX N-PSDB; ABS68606.
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX Example 55; Fig 4; 562pp; English.
 XX The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1P8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
 CC sequence of human immunoglobulin sequence associated with the antibodies
 CC against HDGNR10
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYIVILLNTQEFGLNCS 22
 DB 249 APYIVILLNTQEFGLNCS 270
 RESULT 29
 ABG92880
 ID ABG92880 standard; protein; 352 AA.
 XX ABG92880;
 XX 19-NOV-2002 (first entry)
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.

XX Immunoglobulin; variable heavy chain; variable light chain; human;
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
 KW lymphocytopenia.
 XX
 OS Homo sapiens.
 XX
 XX WO200264612-A2.
 XX
 XX 22-AUG-2002.
 XX
 XX 08-FEB-2002; 2002WO-US003634.
 XX
 XX 09-FEB-2001; 2001US-00779880.
 XX
 XX 09-FEB-2001; 2001WO-US004153.
 XX
 XX 12-JUN-2001; 2001US-0297257P.
 XX
 XX 08-AUG-2001; 2001US-0310458P.
 XX
 XX 12-OCT-2001; 2001US-0328447P.
 XX
 XX 21-DEC-2001; 2001US-0341725P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Roschke V, Rosen CA, Ruben SM;
 XX
 XX WPI; 2002-643455/69.
 XX
 XX N-PSDB; ABS68553.
 XX
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for
 PT treating, preventing, ameliorating or monitoring diseases or disorders
 PT associated with aberrant expression of HDGNR10 e.g. cancer.
 XX
 XX Disclosure; Fig 1A-B; 562pp; English.
 PS
 XX The invention describes an isolated polynucleotide encoding a first
 CC antibody at least 95-100% identical to a second antibody consisting of an
 CC amino acid sequence comprising at least one, two or three CDR regions of
 CC a variable heavy (VH) or variable light (VL) domain of the antibody
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.D5, XF27/28.18B5,
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
 CC is useful treating, preventing, ameliorating, prognosing or monitoring
 CC cancers or other diseases or disorders e.g. immunologic deficiency
 CC syndromes such as blood protein disorders and ataxia telangiectasia,
 CC inflammation associated disorders such as endotoxin lethality, nephritis
 CC and inflammatory bowel disease, conditions associated with an increase in
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant
 CC chemotaxis of immune cells or i-cell antigen presenting cell interaction,
 CC an infectious disease, an autoimmune disease such as Addison's disease,
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
 CC disease or disorder associated with aberrant expression of novel human G-
 CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence
 CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNVLLNTFQEFGLNCS 22
 DB 249 APYNVLLNTFQEFGLNCS 270
 Search completed: March 4, 2004, 17:59:24
 Job time : 53.3061 secs

RESULT 30
 AAE25808
 ID AAE25808 standard; protein; 352 AA.
 XX
 AC AAE25808;
 XX
 DT 24-FEB-2003 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;
 KW hyperproliferative disease; receptor.
 XX
 OS Homo sapiens.
 XX
 XX US2002061834-A1.
 XX
 XX 23-MAY-2002.
 XX
 XX 09-FEB-2001; 2001US-00779880.
 XX
 XX 09-FEB-2000; 2000US-0181258P.
 XX
 XX 09-MAR-2000; 2000US-0187999P.
 XX
 XX 22-SEP-2000; 2000US-0234336P.
 XX
 XX (ROSE/) ROSEN C A.
 XX
 XX (ROSC/) ROSCHKE V.
 XX
 XX (LIYY/) LI Y.
 XX
 XX (RUBE/) RUBEN S M.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX
 XX WPI; 2002-499674/53.
 XX
 XX N-PSDB; RAD42409.
 XX
 XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also
 PT related antibodies.
 XX
 XX Claim 61; Page 163-164; 186pp; English.
 PS
 CC The invention relates to human G-protein chemokine receptor (CCR5),
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5
 CC antibodies are used for the treatment or prevention of inflammation,
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-
 CC presenting cell interaction, viral infections (specifically human immune
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis
 CC carinii infection, Kaposi's sarcoma or any condition associated with the
 CC aberrant expression of CCR5 or their ligands. They are also used for the
 CC detection, diagnosis, prognosis and monitoring of cancers or other
 CC hyperproliferative diseases. The present sequence is human G-protein
 CC chemokine receptor (CCR5), HDGNR10 DNA
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 118; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNVLLNTFQEFGLNCS 22
 DB 249 APYNVLLNTFQEFGLNCS 270
 Search completed: March 4, 2004, 17:59:24
 Job time : 53.3061 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 11.2245 Seconds
(without alignments)
188.535 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYINVILLNTQFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	100.0	352	A43113	chemokine (C-C) re
2	103	87.3	360	JC2443	chemokine (C-C) re
3	103	87.3	374	I38450	chemokine (C-C) re
4	70	59.3	344	J05942	chemokine receptor
5	56	47.5	355	A51177	chemokine (C-C) re
6	54.5	46.2	1075	T07448	probable DNA-direc
7	53	44.9	360	A57160	chemokine (C-C) re
8	52	44.1	355	G02436	chemokine (C-C) re
9	52	44.1	360	JC4587	chemokine (C-C) re
10	52	44.1	383	S55594	G protein-coupled
11	52	44.1	466	JH0197	muscarinic acetyl
12	52	44.1	466	S10126	muscarinic acetyl
13	52	44.1	466	S10856	muscarinic acetyl
14	52	44.1	466	A27386	muscarinic acetyl
15	51	43.2	589	A29476	muscarinic acetyl
16	50	42.4	490	A35546	muscarinic acetyl
17	48	40.7	294	A29337	hypothetical prote
18	48	40.7	300	H98344	hypothetical prote
19	48	40.7	342	G69502	histidinol-phospha
20	48	40.7	359	I49341	MIP-1 alpha recept
21	48	40.7	484	A48657	muscarinic acetyl
22	48	40.7	589	B29514	muscarinic acetyl
23	48	40.7	590	S10128	muscarinic acetyl
24	48	40.7	590	S01114	muscarinic acetyl
25	48	40.7	590	S47572	muscarinic acetyl
26	48	40.7	639	A5019	muscarinic acetyl
27	47	39.8	352	B69901	fatty-acid desatur
28	47	39.8	478	C29514	muscarinic acetyl
29	47	39.8	479	S10127	muscarinic acetyl

muscarinic acetyl
probable sugar tra
hypothetical prote
glutamine ABC tran
macrophage inflam
G protein-coupled
G protein-coupled
hypothetical prote
DNA-directed RNA p
hypothetical prote
probable G protein
G protein-coupled
pentamidine resist
guanylate cyclase
guanylate cyclase
guanylate cyclase
hypothetical prote
NADH dehydrogenase
muscarinic acetyl
preprotein translo
preprotein translo
histidinol-phospha
hypothetical prote
conserved hypotet
NADH2 dehydrogenas
MDCR15 protein - h
G protein-coupled
neurokinin 2 recep
neurokinin 2 recep
neurokinin 2 recep
CDP-4-keto-6-deoxy
CDP-4-keto-6-deoxy
probable CDP-4-ket
probable dehydrata
muscarinic acetyl
muscarinic acetyl
muscarinic acetyl
muscarinic acetyl
muscarinic recepto
muscarinic acetyl
muscarinic acetyl
hypothetical prote
hypothetical prote
DNA-directed RNA p
DNA-directed RNA p
probable membrane
YJX protein - Esc
hypothetical prote
hypothetical prote
sugar transporter-
lipoxigenase (EC 1
probable DNA-direc
probable outer mem
myosin-2 isoform -
probable membrane
gene 9 protein - p
major facilitator
hypothetical prote
hypothetical prote
protein F17L21.16
cyclic nucleotide
hypothetical prote
cytochrome C oxida
hypothetical prote
hypothetical prote
hypothetical prote
alcohol dehydrogen
glutamyl-tRNA redu
hypothetical prote
protoporphyrinogen

ALIGNMENTS

RESULT 1
A43113
chemokine (C-C) receptor 5 - human
N;Alternate names: C-C CKR-5; CCR5
C;Species: Homo sapiens (man)
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
C;Accession: A43113; S71808; A58834; A58832; G02653; A58833
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A;Reference number: A43113; MUID:96241590; PMID:8639485
A;Accession: A43113
A;Molecule type: mRNA
A;Residues: 1-352 <SAM1>
A;Cross-references: GB:X91492; NID:gl1262810; PIDN:CAAG2796.1; PID:gl1262811
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Lienard, C.; Farber, C.M.; Saragosti
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.
Nature 382, 722-725, 1996
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the *CCR5* gene
A;Reference number: S71808; MUID:96345670; PMID:8751444
A;Accession: S71808
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 182-206;207-230 <SAM2>
A;Accession: A58834
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-184; 185-206;207-230 <SAM3>
A;Cross-references: GB:X99393; NID:gl1524062; PIDN:CAAG67767.1; PID:gl1524063
A;Note: This frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection
R;Lebedev, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor
A;Reference number: A58832; MUID:96295970; PMID:8699119
A;Accession: A58832
A;Molecule type: mRNA
A;Residues: 1-352 <COM1>
A;Cross-references: GB:U57840; PIDN:AA817071.1; PID:gl1502409
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R;Comadriere, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: H01541
A;Accession: G02653
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-89; 91-352 <COM2>
A;Cross-references: EMBL:U57840
R;Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor
A;Reference number: A58833; MUID:96291862; PMID:8663314
A;Accession: A58833
A;Molecule type: mRNA
A;Residues: 1-352 <RAP>
A;Cross-references: GB:U54994; PIDN:AA050598.1; PID:gl1457946
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine receptor and MIP-1alpha
C;Genetics:
A;Gene: GDB:CMKBR5; CCR5; CC-CKR-5; CCR5; ChemR13
A;Cross-references: GDB:1230510; OMIM:601373
A;Map position: 3p21-3p21
C;Function:
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A;Note: probably acts to control granulocyte proliferation and differentiation
C;Superfamily: vertebrate rhodopsin
C;Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;32-56/Domain: transmembrane #status predicted <TM1>
F;67-87/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>

F;142-166/Domain: transmembrane #status predicted <TM4>
F;193-218/Domain: transmembrane #status predicted <TM5>
F;236-257/Domain: transmembrane #status predicted <TM6>
F;285-300/Domain: transmembrane #status predicted <TM7>
F;20-269,101-178/Disulfide bonds: #status predicted
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 118; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYIVILLNTFOEFFGLNCS 22
Db 249 APYIVILLNTFOEFFGLNCS 270

RESULT 2
JC2443
chemokine (C-C) receptor 2, splice form B - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1995 #sequence revision 05-Apr-1995 #text change 20-Jun-2000
C;Accession: JC2443; I38463
R;Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A;Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1
A;Reference number: JC2443; MUID:94324942; PMID:8048929
A;Accession: JC2443
A;Molecule type: mRNA
A;Residues: 1-360 <YAM>
A;Cross-references: DDBJ:D29984; NID:gs31246; PIDN:BAAG6253.1; PID:gs31247
R;Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
A;Reference number: A53477; MUID:94195821; PMID:8146186
A;Accession: I38463
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U03905; NID:gs472557; PIDN:AAAL9120.1; PID:gs472558
C;Genetics:
A;Gene: GDB:CMKBR2
A;Cross-references: GDB:337364; OMIM:601267
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
F;43-70/Domain: transmembrane #status predicted <TM1>
F;81-100/Domain: transmembrane #status predicted <TM2>
F;115-136/Domain: transmembrane #status predicted <TM3>
F;154-178/Domain: transmembrane #status predicted <TM4>
F;207-226/Domain: transmembrane #status predicted <TM5>
F;244-268/Domain: transmembrane #status predicted <TM6>
F;287-309/Domain: transmembrane #status predicted <TM7>
F;14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;113-190/Disulfide bonds: #status predicted

Query Match 87.3%; Score 103; DB 2; Length 360;
Best Local Similarity 90.0%; Pred. No. 9.3e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PYIVILLNTFOEFFGLNCS 21
Db 258 PYIVILLNTFOEFFGLNCS 277

RESULT 3
I38450
chemokine (C-C) receptor 2, splice form A - human
N;Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence revision 16-Feb-1996 #text change 13-Aug-1999

RESULT 7
A57160

```

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-261/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:324-273,106-183/Disulfide bonds: #status predicted <TM7>
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 355;
Best Local Similarity 40.0%; Pred. No. 1.4;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNCC 21
|||:||||:|:|
DB 254 PYNVAILLSYQILFGNDC 273

RESULT 9
UC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: J04587
B:Biogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A:Reference number: J04587; MUID:96136324; PMID:8573157
A:Accession: J04587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>
A:Cross-references: EMBL:X90862; NID:gil167851; PIDN:CAA62372.1; PID:gil167852
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
A:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:72,202,350/Binding site: carbohydrate (Aan) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:7321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 360;
Best Local Similarity 47.6%; Pred. No. 1.5;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNCC 22
|||:||||:|:|
DB 257 PYNVLFLETLVELEVLQDCT 277

RESULT 10
S55594
G protein-coupled receptor E1 - equine herpesvirus 2
C:Species: equine herpesvirus 2
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S55594
R:J. Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
J. Mol. Biol. 249, 520-528, 1995
A:Title: The DNA sequence of equine herpesvirus 2.
A:Reference number: S55594; MUID:95302501; PMID:7783207
A:Accession: S55594
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-383 <TEL>
A:Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor
Query Match 44.1%; Score 52; DB 2; Length 383;
Best Local Similarity 90.9%; Pred. No. 1.6;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

```

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNVILLNTF 12
 |||||:|:|
 Db 293 PYNVILLSTF 303

RESULT 11

muscarinic acetylcholine receptor M2 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Nov-1999
 C:Accession: J0197; D37121
 R:Rial, J.; Bloom, J.W.; Yamamura, H.I.; Roeske, W.R.
 Life Sci. 47, 1001-1013, 1990
 A>Title: Amplification of the rat m2 muscarinic receptor gene by the polymerase chain reaction
 A:Reference number: J0197; MUID:91041524; PMID:2172674
 A:Accession: J0197
 A:Molecule type: DNA
 A:Residues: 1-466 <LAI>
 R:Kuttenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
 J. Biol. Chem. 265, 13702-13708, 1990
 A>Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues involved in agonist recognition
 A:Reference number: A37121; MUID:90337982; PMID:2380182
 A:Accession: D37121
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 60-122 <KUR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
 F:23-48/Domain: transmembrane #status predicted <TM1>
 F:61-85/Domain: transmembrane #status predicted <TM2>
 F:98-119/Domain: transmembrane #status predicted <TM3>
 F:139-162/Domain: transmembrane #status predicted <TM4>
 F:184-207/Domain: transmembrane #status predicted <TM5>
 F:389-409/Domain: transmembrane #status predicted <TM6>
 F:421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTF 12
 |||||:|:|
 Db 401 APYNVWVLIINTF 412

RESULT 12

muscarinic acetylcholine receptor M2 - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999
 C:Accession: S10126
 R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.
 EMBO J. 6, 3923-3929, 1987
 A>Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of human muscarinic acetylcholine receptor subtypes
 A:Reference number: S04326; MUID:88166632; PMID:3443095
 A:Accession: S10126
 A:Molecule type: DNA
 A:Residues: 1-466 <PER>
 A:Cross-references: EMBL:X15264; NID:g32319; PIDN:CAA33335.1; PID:g32320
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase
 F:23-48/Domain: transmembrane #status predicted <TM1>
 F:60-89/Domain: transmembrane #status predicted <TM2>
 F:98-119/Domain: transmembrane #status predicted <TM3>
 F:139-162/Domain: transmembrane #status predicted <TM4>
 F:184-207/Domain: transmembrane #status predicted <TM5>
 F:389-409/Domain: transmembrane #status predicted <TM6>
 F:421-442/Domain: transmembrane #status predicted <TM7>
 F:2,6,9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 466;

Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTF 12
 |||||:|:|
 Db 401 APYNVWVLIINTF 412

RESULT 13

muscarinic acetylcholine receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
 C:Accession: S10856
 R:Gocayne, J.; Robinson, D.A.; FitzGerald, M.G.; Chung, F.Z.; Kerlavage, A.R.; Lentes, K.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8296-8300, 1987
 A>Title: Primary structure of rat cardiac beta-adrenergic and muscarinic cholinergic receptors
 A:Reference number: S10855; MUID:88068581; PMID:2825184
 A:Accession: S10856
 A:Molecule type: mRNA
 A:Residues: 1-466 <GOC>
 A:Cross-references: EMBL:J03025; NID:g203461; PIDN:AAA40926.1; PID:g203462
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase
 F:23-48/Domain: transmembrane #status predicted <TM1>
 F:61-85/Domain: transmembrane #status predicted <TM2>
 F:98-119/Domain: transmembrane #status predicted <TM3>
 F:139-162/Domain: transmembrane #status predicted <TM4>
 F:184-207/Domain: transmembrane #status predicted <TM5>
 F:389-409/Domain: transmembrane #status predicted <TM6>
 F:421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;
 Best Local Similarity 66.7%; Pred. No. 1.9;
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTF 12
 |||||:|:|
 Db 401 APYNVWVLIINTF 412

RESULT 14

muscarinic acetylcholine receptor, cardiac - pig
 N:Alternate names: muscarinic acetylcholine receptor M2
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2000
 C:Accession: A27386; A25656
 R:Peralta, E.G.; Winslow, J.W.; Peterson, G.L.; Smith, D.H.; Ashkenazi, A.; Ramachandran, J.
 Science 236, 600-605, 1987
 A>Title: Primary structure and biochemical properties of an M-2 muscarinic receptor.
 A:Reference number: A27386; MUID:87206169; PMID:3107123
 A:Accession: A27386
 A:Molecule type: DNA; mRNA
 A:Residues: 1-466 <PER>
 A:Cross-references: GB:M16331; NID:g164311; PIDN:AAA30986.1; PID:g164313
 A:Experimental source: atrial muscle
 A>Note: the protein sequence derived from the mRNA clones differs from that of the genome
 R:Castro, J.
 FEBS Lett. 209, 367-372, 1986
 A>Title: Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced from complementary DNA
 A:Reference number: A25656; MUID:87080790; PMID:3792556
 A:Accession: A25656
 A:Molecule type: mRNA
 A:Residues: 1-329, 'K', 331-466 <KUB>
 A:Cross-references: GB:X04708; NID:g1859; PIDN:CAA28413.1; PID:g1860
 A:Experimental source: cardiac muscle
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: cardiac muscle; G protein-coupled receptor; glycoprotein; heart; neurotransmitter
 F:23-48/Domain: transmembrane #status predicted <TM1>
 F:61-85/Domain: transmembrane #status predicted <TM2>
 F:98-119/Domain: transmembrane #status predicted <TM3>
 F:139-162/Domain: transmembrane #status predicted <TM4>


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E;184-207/Domain: transmembrane #status predicted <TM5>
F;389-409/Domain: transmembrane #status predicted <TM6>
F;421-442/Domain: transmembrane #status predicted <TM7>

Query Match      44.1%; Score 52; DB 2; Length 466;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTF 12
    |||:::|:|
Db 401 APYNVLLNTF 412

RESULT 15
A29476
muscarinic acetylcholine receptor M4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Feb-2000
C;Accession: A29476
R;Braun, T.; Schofield, P.R.; Shivers, B.D.; Pritchett, D.B.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 149, 125-132, 1987
A;Title: A novel subtype of muscarinic receptor identified by homology screening.
A;Reference number: A29476; MUID: 88077068; PMID: 3120722
A;Accession: A29476
A;Molecule type: mRNA
A;Residues: 1-589 <BRA>
A;Cross-references: GB:M18088; NID: g202657; PIDN: AAA40659.1; PID: g202658
A;Experimental source: brain
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
F;67-90/Domain: transmembrane #status predicted <TM1>
F;104-124/Domain: transmembrane #status predicted <TM2>
F;142-163/Domain: transmembrane #status predicted <TM3>
F;184-206/Domain: transmembrane #status predicted <TM4>
F;230-251/Domain: transmembrane #status predicted <TM5>
F;492-512/Domain: transmembrane #status predicted <TM6>
F;527-545/Domain: transmembrane #status predicted <TM7>

Query Match      43.2%; Score 51; DB 2; Length 589;
Best Local Similarity 61.5%; Pred. No. 3.5;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNVLVNTFRD 517
    |||:::|:|
Db 505 PYNVLVNTFRD 517

RESULT 16
A35546
muscarinic acetylcholine receptor M4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jul-2000
C;Accession: A35546
R;Tietje, K.M.; Goldman, P.S.; Nathanson, N.M.
J. Biol. Chem. 265, 2828-2834, 1990
A;Title: Cloning and functional analysis of a gene encoding a novel muscarinic acetylcholine
A;Reference number: A35546; MUID: 90153912; PMID: 2154460
A;Accession: A35546
A;Molecule type: DNA
A;Residues: 1-490 <TIE>
A;Cross-references: GB:J05218; NID: g211067; PIDN: AAA48563.1; PID: g211068
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane
F;42-67/Domain: transmembrane #status predicted <TM1>
F;80-104/Domain: transmembrane #status predicted <TM2>
F;117-138/Domain: transmembrane #status predicted <TM3>
F;158-181/Domain: transmembrane #status predicted <TM4>
F;203-226/Domain: transmembrane #status predicted <TM5>
F;413-433/Domain: transmembrane #status predicted <TM6>
F;445-466/Domain: transmembrane #status predicted <TM7>

Query Match      42.4%; Score 50; DB 2; Length 490;
Best Local Similarity 61.5%; Pred. No. 4.2;

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Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 PYNVLVNTFRD 14
    |||:::|:|
Db 426 PYNVLVNTFRD 438

RESULT 17
AG2937
hypothetical protein Atu3101 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AG2937
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell.
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID: 21608550; PMID: 11743193
A;Accession: AG2937
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <KUR>
A;Cross-references: GB:AE008689; PIDN: AAL43917.1; PID: g17741468; GSPDB: GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3101
A;Map position: linear chromosome
C;Superfamily: inner membrane protein ugpA

Query Match      40.7%; Score 48; DB 2; Length 294;
Best Local Similarity 52.4%; Pred. No. 5.2;
Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 2 PYN--IVLLNTFRPFGLNN 20
    |:| |||:::|:|
Db 242 PFNSSFVLLKVTREAFQLNN 262

RESULT 18
H98344
hypothetical protein AGR_L3415 [imported] - Agrobacterium tumefaciens (strain C58, Cert
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: H98344
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur
A;Reference number: A97359; MUID: 21608551; PMID: 11743194
A;Accession: H98344
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <KUR>
A;Cross-references: GB:AE007870; PIDN: AAK90282.1; PID: g15160307; GSPDB: GN00170
C;Genetics:
A;Gene: AGR_L3415
A;Map position: linear chromosome
C;Superfamily: inner membrane protein ugpA

Query Match      40.7%; Score 48; DB 2; Length 300;
Best Local Similarity 52.4%; Pred. No. 5.4;
Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 2 PYN--IVLLNTFRPFGLNN 20
    |:| |||:::|:|
Db 248 PFNSSFVLLKVTREAFQLNN 268

RESULT 19
G69502

```

histidinol-phosphate aminotransferase (hisC-2) homolog - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
 C:Accession: G69502
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: G69502
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-342 <KJE>
 C:Cross-references: GB:AE000963; GB:AE000782; NID:G2689286; PIDN:AA089229.1; PID:G264851
 C:Superfamily: probable histidinol-phosphate transaminase

Query Match 40.7%; Score 48; DB 2; Length 342;
 Best Local Similarity 50.0%; Pred. No. 6.1;
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 YNIVLLNTFOEFFGL 18
 |||:::|:|:|
 Db 195 YNNLVLSFSGFGL 210

RESULT 20
 I49341
 MIP-1 alpha receptor like-2 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
 C:Accession: I49341
 R:Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A>Title: Cloning and differential tissue-specific expression of three mouse beta chemoki
 A:Reference number: I49339; MUID:95340546; PMID:7542241
 A:Accession: I49341
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <RES>
 C:Cross-references: EMBL:U28406; NID:9881551; PID:G881552
 C:Superfamily: vertebrate rhodopsin

Query Match 40.7%; Score 48; DB 2; Length 359;
 Best Local Similarity 45.0%; Pred. No. 6.4;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNMC 21
 |||:::|:|:|
 Db 258 PYNVLVLSAFHSTFLETSC 277

RESULT 21
 S48657
 muscarinic acetylcholine receptor MR - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S48657; S24948
 R:Herrera, L.; Carvallo, P.; Antonelli, M.; Olate, J.
 FEBS Lett. 352, 175-179, 1994
 A>Title: Cloning of a Xenopus laevis muscarinic receptor encoded by an intronless gene.
 A:Reference number: S48657; MUID:95010703; PMID:7925970
 A:Accession: S48657
 A:Molecule type: mRNA
 A:Residues: 1-484 <HEH>
 C:Cross-references: GB:X65865; NID:G64900; PIDN:CAA46694.1; PID:G64901
 R:Olate, J.
 submitted to the EMBL Data Library, April 1992
 A:Reference number: S24948
 A:Accession: S24948
 A:Molecule type: mRNA

A:Residues: 1-131, 'X', 133-484 <OLA>
 A:Cross-references: EMBL:X65865; NID:G64900; PID:G64901
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
 F:33-58/Domain: transmembrane #status predicted <TM1>
 F:71-95/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:149-172/Domain: transmembrane #status predicted <TM4>
 F:194-217/Domain: transmembrane #status predicted <TM5>
 F:407-427/Domain: transmembrane #status predicted <TM6>
 F:439-460/Domain: transmembrane #status predicted <TM7>

Query Match 40.7%; Score 48; DB 2; Length 484;
 Best Local Similarity 63.6%; Pred. No. 8.7;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
 |||:::|:|:|
 Db 420 PYNMVLINTF 430

RESULT 22
 B29514
 muscarinic acetylcholine receptor M3 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Feb-2000
 C:Accession: B94518; B94293; B37121; B29514
 R:Bonner, T.I.
 submitted to GenBank, July 1987
 A:Reference number: A94518
 A:Accession: B94518
 A:Molecule type: mRNA
 A:Residues: 1-589 <BO1>
 R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
 Science 237, 527-532, 1987
 A>Title: Identification of a family of muscarinic acetylcholine receptor genes.
 A:Reference number: A94293; MUID:97263421; PMID:3037705
 A:Accession: B94293
 A:Molecule type: mRNA
 A:Residues: 1-269; 463-589 <BO2>
 A:Experimental source: cerebral cortex
 A>Note: only a part of the protein translation is given; none of the nucleotide sequence
 R:Kurenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Atken, A.; Harris, A.C.M.; Hulme, E.C.
 J. Biol. Chem. 265, 13702-13708, 1990
 A>Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invc
 A:Reference number: A37121; MUID:90337982; PMID:2380182
 A:Accession: B37121
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 104-166 <KUR>
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
 F:67-90/Domain: transmembrane #status predicted <TM1>
 F:104-124/Domain: transmembrane #status predicted <TM2>
 F:142-163/Domain: transmembrane #status predicted <TM3>
 F:184-206/Domain: transmembrane #status predicted <TM4>
 F:230-251/Domain: transmembrane #status predicted <TM5>
 F:492-512/Domain: transmembrane #status predicted <TM6>
 F:527-545/Domain: transmembrane #status predicted <TM7>
 F:6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.7%; Score 48; DB 2; Length 589;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12
 |||:::|:|:|
 Db 505 PYNMVLINTF 515

RESULT 23
 S10128
 muscarinic acetylcholine receptor M4 - human

C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Feb-2000
 C/Accession: S10128
 R/Beralt, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.D.
 EMO J. 6, 3923-3929, 1987
 A/Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of two distinct subtypes of the human 5-HT₂ receptor
 A/Reference number: S04326; MUID:98166632; PMID:3443095
 A/Accession: S10128
 A/Molecule type: DNA
 A/Residues: 1-590 <PER>
 A/Cross-references: EMBL:X15266; NID:g32323; PIDN:CAA33337.1; PID:g32324
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein; transmembrane domain; transmembrane status predicted <TM1>
 F/105-131/Domain: transmembrane #status predicted <TM2>
 F/143-164/Domain: transmembrane #status predicted <TM3>
 F/185-207/Domain: transmembrane #status predicted <TM4>
 F/231-252/Domain: transmembrane #status predicted <TM5>
 F/493-513/Domain: transmembrane #status predicted <TM6>
 F/525-546/Domain: transmembrane #status predicted <TM7>
 F/5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12
 |||||:|:|
 Db 506 PYNIMVLVNTFF 516

RESULT 24
 S01114
 muscarinic acetylcholine receptor M2, glandular - pig
 N/Alternate names: muscarinic acetylcholine receptor III
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Feb-2000
 C/Accession: S01114
 R/Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.
 FEBS Lett. 235, 257-261, 1988
 A/Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonists
 A/Reference number: S01114; MUID:98296835; PMID:3402600
 A/Accession: S01114
 A/Molecule type: DNA
 A/Residues: 1-590 <AKI>
 A/Cross-references: EMBL:X12712; NID:g1861; PIDN:CAA31215.1; PID:g1862
 C/Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein; transmembrane domain; transmembrane status predicted <TM1>
 F/105-125/Domain: transmembrane #status predicted <TM2>
 F/143-164/Domain: transmembrane #status predicted <TM3>
 F/185-207/Domain: transmembrane #status predicted <TM4>
 F/231-252/Domain: transmembrane #status predicted <TM5>
 F/493-513/Domain: transmembrane #status predicted <TM6>
 F/528-546/Domain: transmembrane #status predicted <TM7>

Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12
 |||||:|:|
 Db 506 PYNIMVLVNTFF 516

RESULT 25
 S47572
 muscarinic acetylcholine receptor m3 - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Feb-2000
 C/Accession: S47572
 R/Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.
 Biochim. Biophys. Acta 1223, 151-154, 1994

A/Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 r
 A/Reference number: S47572; MUID:94339178; PMID:8061048
 A/Accession: S47572
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-590 <LEE>
 A/Cross-references: EMBL:U08286; NID:g520465; PIDN:AAA51866.1; PID:g520466
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: neurotransmitter receptor

Query Match 40.7%; Score 48; DB 2; Length 590;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12
 |||||:|:|
 Db 506 PYNIMVLVNTFF 516

RESULT 26
 A55019
 muscarinic acetylcholine receptor, M3 isoform - chicken
 C/Species: Gallus gallus (chicken)
 C/Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000
 C/Accession: A55019
 R/Gadbut, A.P.; Galper, J.B.
 J. Biol. Chem. 269, 25823-25829, 1994
 A/Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and ventricle
 A/Reference number: A55019; MUID:95014393; PMID:7929287
 A/Accession: A55019
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-639 <GAD>
 A/Cross-references: GB:I10617; NID:g530097; PIDN:AAA65961.1; PID:g530098
 C/Superfamily: vertebrate rhodopsin
 C/Keywords: neurotransmitter receptor

Query Match 40.7%; Score 48; DB 2; Length 639;
 Best Local Similarity 72.7%; Pred. No. 12;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12
 |||||:|:|
 Db 556 PYNIMVLVNTFF 566

RESULT 27
 B69901
 fatty-acid desaturase homolog yocE - Bacillus subtilis
 C/Species: Bacillus subtilis
 C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C/Accession: B69901
 R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte, I.; Boehm, J.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eyring, J.; Fabbri, C.; Ferrai, E.; Nature 390, 249-256, 1997
 A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle, Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Fortetelli, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, T. A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A/Reference number: A69580; MUID:98044033; PMID:9384377
 A/Accession: B69901
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-352 <KUN>
 A/Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13810.1; PID:g2634311

A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yocE
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 39.8%; Score 47; DB 2; Length 352;
 Best Local Similarity 60.0%; Pred. No. 9.1;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 NIVLLNTFFQFFGL 18
 ::: ||||| |||||
 Db 28 SLQLNTFFPGL 42

RESULT 28

C29514

muscarinic acetylcholine receptor M4 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999

C:Accession: C94518; C94293; E37121; C29514

R:Bonner, T.I.

submitted to GenBank, July 1987

A:Reference number: A94518

A:Accession: C94518

A:Molecule type: mRNA

A:Residues: 1-478 <BO1>

R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.

Science 237, 527-532, 1987

A:Title: Identification of a family of muscarinic acetylcholine receptor genes.

A:Reference number: A94293; MUID:87263421; PMID:3037705

A:Accession: C94293

A:Molecule type: mRNA

A:Residues: 1-233;373-478 <BO2>

A:Experimental source: cerebral cortex

A:Note: only a part of the protein translation is given; none of the nucleotide sequence

R:Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Altken, A.; Harris, A.C.M.; Hulme, E.C.

J. Biol. Chem. 265, 13702-13708, 1990

A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv

A:Reference number: A37121; MUID:90337982; PMID:2380182

A:Accession: E37121

A:Status: preliminary

A:Molecule type: protein

A:Residues: 68-130 <KUR>

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F:31-56/Domain: transmembrane #status predicted <TM1>

F:69-93/Domain: transmembrane #status predicted <TM2>

F:106-127/Domain: transmembrane #status predicted <TM3>

F:147-170/Domain: transmembrane #status predicted <TM4>

F:192-215/Domain: transmembrane #status predicted <TM5>

F:401-421/Domain: transmembrane #status predicted <TM6>

F:433-454/Domain: transmembrane #status predicted <TM7>

F:8.13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.8%; Score 47; DB 2; Length 478;
 Best Local Similarity 63.6%; Pred. No. 12;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNVLLNTFF 12
 |||:::|
 Db 414 PYNVVLTNTF 424

RESULT 29

S10127

muscarinic acetylcholine receptor M3 - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Nov-1999

C:Accession: S10127

R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.

EMBO J. 6, 3923-3929, 1987

A:Title: Distinct primary structures, ligand-binding properties and tissue-specific exp

A:Reference number: S04326; MUID:88166632; PMID:3443095

A:Accession: S10127

A:Molecule type: DNA

A:Residues: 1-479 <PER>

A:Cross-references: EMBL:X15265; NID:g32321; PIDN:CAA33336.1; PID:g32322

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F:32-57/Domain: transmembrane #status predicted <TM1>

F:70-94/Domain: transmembrane #status predicted <TM2>

F:106-128/Domain: transmembrane #status predicted <TM3>

F:148-171/Domain: transmembrane #status predicted <TM4>

F:192-216/Domain: transmembrane #status predicted <TM5>

F:401-422/Domain: transmembrane #status predicted <TM6>

F:433-456/Domain: transmembrane #status predicted <TM7>

F:3.8.13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.8%; Score 47; DB 2; Length 479;

Best Local Similarity 63.6%; Pred. No. 13;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNVLLNTFF 12
 |||:::|
 Db 415 PYNVVLTNTF 425

RESULT 30

S33776

muscarinic acetylcholine receptor m4 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 24-Nov-1999

C:Accession: S33776; S33135

R:van Koppen, C.J.; Lenz, W.; Nathanson, N.M.

Biochim. Biophys. Acta 1173, 342-344, 1993

A:Title: Isolation, sequence and functional expression of the mouse m4 muscarinic acetyl

A:Reference number: S33776; MUID:93305731; PMID:7916637

A:Accession: S33776

A:Molecule type: DNA

A:Residues: 1-479 <KOP>

A:Cross-references: EMBL:X63473; NID:g296913; PIDN:CAA45071.1; PID:g296914

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F:31-56/Domain: transmembrane #status predicted <TM1>

F:69-93/Domain: transmembrane #status predicted <TM2>

F:106-127/Domain: transmembrane #status predicted <TM3>

F:147-170/Domain: transmembrane #status predicted <TM4>

F:192-215/Domain: transmembrane #status predicted <TM5>

F:402-422/Domain: transmembrane #status predicted <TM6>

F:434-455/Domain: transmembrane #status predicted <TM7>

Query Match 39.8%; Score 47; DB 2; Length 479;

Best Local Similarity 63.6%; Pred. No. 13;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNVLLNTFF 12
 |||:::|
 Db 415 PYNVVLTNTF 425

Search completed: March 4, 2004, 18:04:02

Job time : 12.2245 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 7.18367 Seconds
(without alignments)
159.465 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYINVILLNTQFEFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	118	100.0	352	1	CKR5 CERAE
2	118	100.0	352	1	CKR5 CERPY
3	118	100.0	352	1	CKR5 CERTO
4	118	100.0	352	1	CKR5 GORGO
5	118	100.0	352	1	CKR5 HUMAN
6	118	100.0	352	1	CKR5 HYLL
7	118	100.0	352	1	CKR5 HYLL
8	118	100.0	352	1	CKR5 HYLL
9	118	100.0	352	1	CKR5 MACMU
10	118	100.0	352	1	CKR5 PANTR
11	118	100.0	352	1	CKR5 PAPHA
12	118	100.0	352	1	CKR5 PONPY
13	118	100.0	352	1	CKR5 PYGHI
14	118	100.0	352	1	CKR5 PYGNE
15	118	100.0	352	1	CKR5 TRAPH
16	118	100.0	352	1	CKR5 TRAPH
17	108	91.5	354	1	CKR5 MOUSE
18	105	89.0	354	1	CKR5 RAT
19	103	87.3	360	1	CKR2 MACMU
20	103	87.3	374	1	CKR2 HUMAN
21	87	73.7	373	1	CKR2 RAT
22	79	66.9	373	1	CKR2 MOUSE
23	56	47.5	355	1	CKR1 HUMAN
24	54.5	46.2	1075	1	RPOB PINTH
25	53	44.9	360	1	CKR4 HUMAN
26	52	44.1	355	1	CKR3 HUMAN
27	52	44.1	359	1	CKR3 RAT
28	52	44.1	360	1	CKR4 MOUSE
29	52	44.1	440	1	ACM2 PANTR
30	52	44.1	466	1	ACM2 HUMAN
31	52	44.1	466	1	ACM2 MOUSE
32	52	44.1	466	1	ACM2 PIG
33	52	44.1	466	1	ACM2 RAT

P56492 cercopithec
P56483 macaca mula
P56482 macaca mula
P17200 gallus gall
O28255 archaeoglob
P51678 mus musculus
P30544 xenopus lae
Q9er23 mus musculus
P08483 rattus norv
P41984 bos taurus
Q9n2a3 gorilla gor
P20309 homo sapien
Q9n2a4 pan troglod
P11483 sus scrofa
Q9n2a2 pongo pygma
P49578 gallus gall
P08485 rattus norv
P08173 homo sapien
P32211 mus musculus
P51675 mus musculus
Q04683 mus musculus
P34997 rattus norv
P11703 spinacia ol
Q9mtm5 oenothera h
P35411 rattus norv
P51685 homo sapien
O97665 macaca mula
O00590 homo sapien
P38969 saccharomyc
P39432 salmonella
P79880 gallus gall
P43080 homo sapien
P43081 mus musculus
P46065 bos taurus
Q8K912 buchnera ap
P30372 gallus gall
Q9byt8 homo sapien
P47318 mycoplasma
P75559 mycoplasma
P51686 homo sapien
Q92213 cavia porce
Q58365 methanococc
O28220 archaeoglob
P15959 podospora a
P32382 homo sapien
O09027 rattus norv
P05363 bos taurus
P30549 mus musculus
P16610 rattus norv
P26398 salmonella
P11229 homo sapien
P56489 macaca mula
P12657 mus musculus
P04761 sus scrofa
P08482 rattus norv
P08911 rattus norv
P08912 homo sapien
P56490 macaca mula
P52385 human herpe
Q9bb99 lotus japon
P06271 nicotiana t
P50546 arabidopsis
Q8xb14 escherichia
P39411 escherichia
Q8fa41 escherichia
Q9z0d9 mus musculus
P27480 phaeococcus v

ALIGNMENTS

RESULT 1

CKR5 CERAE
ID CKR5 CERAE STANDARD; PRT; 352 AA.
AC P56433;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U83324; AAC51795.1; --
CC EMBL; U83325; AAC51796.1; --
CC EMBL; AB015944; BRA31328.1; --
CC InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR PROSITE; PS50262; G PROTEIN RECP FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

FT VARIANT 14 14 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;
Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4,7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIIVLLNTFOEPPGLNCS 22
DB 249 APYNIIVLLNTFOEPPGLNCS 270
RESULT 2
ID CKR5_CERP STANDARD; PRT; 352 AA.
AC Q9TV42;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=100;
RX MEDLINE=99335215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
AIDS Res. Hum. Retroviruses 15:931-939(1999).
RL -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF035222; AAD44015.1; --
CC InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
DR PROSITE; PS50262; G PROTEIN RECP FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).

```

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
    |||||
DB 249 APYNVLLNTFOEFFGLNCS 270

RESULT 3
CKR5 CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CCRC5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVM isolates use the CCR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVM, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; GPCRIN RECF1.1; 1.
CC PROSITE; PS00262; G PROTEIN RECF1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).

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FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
    |||||
DB 249 APYNVLLNTFOEFFGLNCS 270

RESULT 4
CKR5 GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUN-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CCRC5 OR CMKR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268697; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc Natl Acad Sci U S A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF005659; AAB62553.1; -
CC InterPro: IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRHHODPSN.

```


DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 5 (POTENTIAL).
 FT TRANSMEM 199 218 6 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 7 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40515 MW; D066FCB9FE5EACB4 CRC64;
 Query Match 100.0%; Score 118; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYIVLLNTQFFGLNCS 22
 DB 249 APYIVLLNTQFFGLNCS 270
 RESULT 5
 ID CCR5_HUMAN STANDARD; PRT; 352 AA.
 AC P51681; O14692; O14693; O14696; O14697; O14698; O14699;
 AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
 AC O14708; O15538; Q9UPA4;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
 DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
 GN CCR5 OR CMKBR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96241590; PubMed=8639485;
 RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
 RT "Molecular cloning and functional expression of a new human
 CC chemokine receptor gene";
 RL Biochemistry 35:3362-3367(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96291862; PubMed=8663314;
 RA Raport C.J., Gosling J., Schweighart V.L., Gray P.W., Charo I.F.;
 RT "Molecular cloning and functional characterization of a novel human
 CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha";
 RL J. Biol. Chem. 271:17161-17166(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96295970; PubMed=8699119;
 RA Comadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
 RT "Cloning and functional expression of CC CKR5, a human monocyte CC
 chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
 RANTES";
 RL J. Leukoc. Biol. 60:147-152(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Gao J.L., la Bastide M., Kaplan N., Greco T., Touchman J.,
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
 RA Matanabe M., Doggett N., Garcia D., Sagripanti J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhnman S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses";
 RL J. Virol. 71:8642-8656(1997).
 RN [6]
 RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049523; PubMed=9388201;
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 RT with 5'-end heterogeneity, dual promoter usage, and evidence for
 RT polymorphisms within the regulatory regions and noncoding exons";
 RL J. Biol. Chem. 272:30662-30671(1997).
 RN [8]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
 RA Debre P.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260017; PubMed=8649511;
 RA Deng H., Liu R., Elmeyer W., Choe S., Uemaz D., Burkhardt M.,
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 RT HIV-1";
 RL Nature 381:661-666(1996).
 RN [11]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=96260018; PubMed=8649512;
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 RT CC-CKR-5";
 RL Nature 381:667-673(1996).
 RN [12]
 RP SULFATION.
 RX MEDLINE=99189752; PubMed=10089882;
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 RT entry";
 RL Cell 96:667-676(1999).
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and rantes and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or

CC differentiation. Acts as co-receptor with CD4 for primary non-
CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
CC virus. It promotes Env-mediated fusion of the virus.
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -!- TISSUE SPECIFICITY: Found in promyelocytic cells.
CC
CC -!- PFM: Sulfation contributes to the efficiency of HIV-1 entry.
CC
CC -!- PTM: Modified by O-linked glycosylation, but not by N-linked
CC glycosylation.
CC
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC
CC EMBL; X91492; CAA62796.1; -
CC EMBL; U54994; AAC50598.1; -
CC EMBL; U57840; AAB17071.1; -
CC EMBL; U95626; AAB57793.1; -
CC EMBL; U83326; AAC51797.1; -
CC EMBL; AF011500; AAB65700.1; -
CC EMBL; AF011501; AAB65701.1; -
CC EMBL; AF011502; AAB65702.1; -
CC EMBL; AF011503; AAB65703.1; -
CC EMBL; AF011505; AAB65705.1; -
CC EMBL; AF011506; AAB65706.1; -
CC EMBL; AF011507; AAB65707.1; -
CC EMBL; AF011508; AAB65708.1; -
CC EMBL; AF011509; AAB65709.1; -
CC EMBL; AF011510; AAB65710.1; -
CC EMBL; AF011511; AAB65711.1; -
CC EMBL; AF011512; AAB65712.1; -
CC EMBL; AF011513; AAB65713.1; -
CC EMBL; AF011514; AAB65714.1; -
CC EMBL; AF011515; AAB65715.1; -
CC EMBL; AF011516; AAB65716.1; -
CC EMBL; AF011517; AAB65717.1; -
CC EMBL; AF011518; AAB65718.1; -
CC EMBL; AF011519; AAB65719.1; -
CC EMBL; AF011520; AAB65720.1; -
CC EMBL; AF011521; AAB65721.1; -
CC EMBL; AF011522; AAB65722.1; -
CC EMBL; AF011523; AAB65723.1; -
CC EMBL; AF011524; AAB65724.1; -
CC EMBL; AF011525; AAB65725.1; -
CC EMBL; AF011526; AAB65726.1; -
CC EMBL; AF011527; AAB65727.1; -
CC EMBL; AF011528; AAB65728.1; -
CC EMBL; AF011529; AAB65729.1; -
CC EMBL; AF011530; AAB65730.1; -
CC EMBL; AF011531; AAB65731.1; -
CC EMBL; AF011532; AAB65732.1; -
CC EMBL; AF011533; AAB65733.1; -
CC EMBL; AF011534; AAB65734.1; -
CC EMBL; AF011535; AAB65735.1; -
CC EMBL; AF011536; AAB65736.1; -
CC EMBL; AF011537; AAB65737.1; -
CC EMBL; AF031237; AAB94735.1; -
CC EMBL; AF052539; AAD18131.1; -
CC EMBL; AY221093; AAO65971.1; -
CC Genbank; HGNC:1606; CCR5.
CC
CC MIM; 601373; -
CC
CC GO; GO:0005768; C:cytosol; TAS.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0016493; F:C-C chemokine receptor activity; NAS.
CC GO; GO:0015026; F:coreceptor activity; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0006968; P:cellular defense response; TAS.
CC GO; GO:0006935; P:cytotoxicity; TAS.
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.
DR GO; GO:0007203; P:phosphatidylinositol-4,5-bisphosphate hydro. . .; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNVILLNTFFQFFGLNCS 22
Db 249 APYNVILLNTFFQFFGLNCS 270
|||||

RESULT 6
CKRS_HYLL
ID CKRS_HYLL STANDARD; PRT; 352 AA.
AC O97883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CKCR5.
OS Hylobates leucogenys (White-cheeked gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=61853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC
CC EMBL; AF075451; AAD19863.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).

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FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4,7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
|||||
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 7
CKR5_HYLM
ID CKR5_HYLM STANDARD; PRT; 352 AA.
AC Q95NC0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (CC-CKR-5) (CCR-5) (CCR5).
OS Hylobates moloch (Silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF177899; AAK43382.1; -
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 BY SIMILARITY.
FT DISULFID 101 178 SULFATION (BY SIMILARITY).
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4,7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
|||||
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 8
CKR5_HYLSY
ID CKR5_HYLSY STANDARD; PRT; 352 AA.
AC Q95NC5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=95950;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF177884; AAK43367.1; -
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).

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RT  DOMAIN 125 141  CYTOPLASMIC (POTENTIAL).
FT  TRANSSEM 142 166  4 (POTENTIAL).
FT  DOMAIN 167 198  EXTRACELLULAR (POTENTIAL).
FT  TRANSSEM 199 218  5 (POTENTIAL).
FT  DOMAIN 219 235  CYTOPLASMIC (POTENTIAL).
FT  TRANSSEM 236 260  6 (POTENTIAL).
FT  DOMAIN 261 277  EXTRACELLULAR (POTENTIAL).
FT  TRANSSEM 278 301  7 (POTENTIAL).
FT  DOMAIN 302 352  CYTOPLASMIC (POTENTIAL).
FT  DISULFID 101 178  BY SIMILARITY.
FT  MOD_RES 3 3  SULFATION (BY SIMILARITY).
FT  MOD_RES 10 10  SULFATION (BY SIMILARITY).
FT  MOD_RES 14 14  SULFATION (BY SIMILARITY).
SQ  SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNYVLLNTFQFFGLNCS 22
DB 249 APYNYVLLNTFQFFGLNCS 270

RESULT 9
CKR5 MACMU
ID CKR5 MACMU STANDARD; PRT; 352 AA.
AC P79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RA "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239."
RT J. Virol. 71:2522-2527 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RA "Genetically divergent strains of simian immunodeficiency virus use
RT CKR5 as a coreceptor for entry."
RT J. Virol. 71:2705-2714 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RA "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RN AIDS Res. Hum. Retroviruses 17:981-986 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Feiler S.C., Parmentier M., Broder C.C., Doms R.W.;

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RT  "Differential utilization of CKR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U77672; AAC51109.1; -
CC EMBL; U73739; AAC51158.1; -
CC EMBL; U96782; AAC34132.1; -
CC EMBL; AF005660; AAB62554.1; -
CC EMBL; AF005661; AAB62555.1; -
CC EMBL; AF005662; AAB62556.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1_
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
CC PROSITE; PS00237; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30  EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 31 58  1 (POTENTIAL).
FT DOMAIN 59 68  CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 69 89  2 (POTENTIAL).
FT DOMAIN 90 102  EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 103 124  3 (POTENTIAL).
FT DOMAIN 125 141  CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 142 166  4 (POTENTIAL).
FT DOMAIN 167 198  EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 199 218  5 (POTENTIAL).
FT DOMAIN 219 235  CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 236 260  6 (POTENTIAL).
FT DOMAIN 261 277  EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 278 301  7 (POTENTIAL).
FT DOMAIN 302 352  CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178  BY SIMILARITY.
FT MOD_RES 3 3  SULFATION (BY SIMILARITY).
FT MOD_RES 10 10  SULFATION (BY SIMILARITY).
FT MOD_RES 14 14  SULFATION (BY SIMILARITY).
FT MOD_RES 15 15  SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268  N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 241 241  M -> I (IN REF. 3).
FT CONFLICT 292 292  I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNYVLLNTFQFFGLNCS 22
DB 249 APYNYVLLNTFQFFGLNCS 270

RESULT 10
CKR5 PANTR
ID CKR5 PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

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GN CCR5 OR CMKRS.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [4]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97426118; PubMed=9282822;
 RA Zacharova V., Zachar V., Goustin A.S.;
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 RT HIV type 1 host.";
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 RN [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98090115; PubMed=9430250;
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 RN [6]
 RN SEQUENCE FROM N.A.
 RX Zhang Y., Ryder O.A., Zhang Y.;
 RT "Sequence comparison of the CCR5 gene in primates and primate
 RT phylogeny.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC or send an email to license@sib-sib.ch)
 CC
 CC EMBL; AF005663; AAB62557.1; -
 CC EMBL; U94329; AAB58446.1; -
 CC EMBL; AF011542; AAB65742.1; -
 CC EMBL; U97666; AAC51670.1; -
 CC EMBL; AF011540; AAB65740.1; -
 CC EMBL; U89797; AAC03717.1; -
 CC EMBL; AF17894; AAK43377.1; -
 CC InterPro; IPR000276; GPCR_Rhodopsin.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsin.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 89
 FT DOMAIN 90 102
 FT TRANSMEM 103 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 166
 FT DOMAIN 167 198
 FT TRANSMEM 199 218
 FT DOMAIN 219 235
 FT TRANSMEM 236 260
 FT DOMAIN 261 277
 FT TRANSMEM 278 301
 FT DOMAIN 302 352
 FT DISULFID 101 178
 FT MOD_RES 3 3
 FT MOD_RES 10 10
 FT MOD_RES 14 14
 FT MOD_RES 15 15
 FT CARBOHYD 268 268
 FT CONFLICT 123 123
 FT SEQUENCE 352 AA; 40539 MW; 4A3B698B80FE34C CRC64;
 SQ
 Query Match 100.0%; Score 118; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. NO. 4.7e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYNVILLNTQEFGLNCS 22
 DB 249 APYNVILLNTQEFGLNCS 270
 RESULT 11
 CCR5_PAPHA
 ID CCR5_PAPHA STANDARD; PRT; 352 AA.
 AC P56441;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR5) (CC-CCR5) (CCR-5) (CCRS).
 GN CCR5 OR CMKRS.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Papio.
 OX NCBI_TaxID=9557, 9555;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP SPECIES=P.hamadryas;
 RX Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RX Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RX Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP SPECIES=P.hamadryas;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP SPECIES=P.hamadryas;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Saksena N.K., Wang B., Bolton W., Smit T.K., Lal R.B.;
 RT "Species-specific changes in the CCR5 gene from African and Asian
 RT nonhuman primates.";
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP SPECIES=P.anubis;
 RA Benton P.A., Timanov D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF005658; AAB2352.1; -
 CC EMBL; AF105287; AAD20556.1; -
 CC EMBL; AF105288; AAD20557.1; -
 CC EMBL; AF105289; AAD20558.1; -
 CC EMBL; AF105290; AAD20559.1; -
 CC EMBL; AF023452; AAC63830.1; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.

CC Pfam; PF00001; 7tm_1; 1.

CC PRINTS; PR00237; GPCRHHODPSN.

CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 31 58 1 (POTENTIAL).

CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 59 89 2 (POTENTIAL).

CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 103 124 3 (POTENTIAL).

CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 142 166 4 (POTENTIAL).

CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 199 218 5 (POTENTIAL).

CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 236 260 6 (POTENTIAL).

CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 278 301 7 (POTENTIAL).

CC DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

CC DISULFID 101 178 BY SIMILARITY.

CC MOD RES 3 3 SULFATION (BY SIMILARITY).

CC MOD RES 10 10 SULFATION (BY SIMILARITY).

CC MOD RES 14 14 SULFATION (BY SIMILARITY).

CC MOD RES 15 15 SULFATION (BY SIMILARITY).

CC CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).

CC SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1F5B2 CRC64;

CC Query Match 100.0%; Score 118; DB 1; Length 352;

CC Best Local Similarity 100.0%; Pred. No. 4.7e-11;

CC Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RX MEDLINE=99416438; PubMed=10486970;

RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

RI "Sequence evolution of the CCR5 chemokine receptor gene in primates.";

RL Mol. Biol. Evol. 16:1145-1154 (1999).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role

CC in the control of granulocytic lineage proliferation or

CC differentiation.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF075446; AAD19858.1; -

CC InterPro: IPR000276; GPCR_Rhodopsn.

CC Pfam; PF00001; 7tm_1; 1.

CC PRINTS; PR00237; GPCRHHODPSN.

CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 31 58 1 (POTENTIAL).

CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 59 89 2 (POTENTIAL).

CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 103 124 3 (POTENTIAL).

CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 142 166 4 (POTENTIAL).

CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 199 218 5 (POTENTIAL).

CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 236 260 6 (POTENTIAL).

CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

CC TRANSMEM 278 301 7 (POTENTIAL).

CC DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

CC DISULFID 101 178 BY SIMILARITY.

CC MOD RES 3 3 SULFATION (BY SIMILARITY).

CC MOD RES 10 10 SULFATION (BY SIMILARITY).

CC MOD RES 14 14 SULFATION (BY SIMILARITY).

CC MOD RES 15 15 SULFATION (BY SIMILARITY).

CC SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

CC Query Match 100.0%; Score 118; DB 1; Length 352;

CC Best Local Similarity 100.0%; Pred. No. 4.7e-11;

CC Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13

CKR5_PONY

ID CKR5_PONY

AC 097881;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

GN CCR5 OR CMKRS.

OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.

OC NCBI_TaxID=9600;

OX [1]

RP SEQUENCE FROM N.A.

RN

[1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS02622; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC DOMAIN 167 198 5 (POTENTIAL).
CC TRANSMEM 199 218 6 (POTENTIAL).
CC DOMAIN 219 235 7 (POTENTIAL).
CC TRANSMEM 236 260 8 (POTENTIAL).
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 278 302 9 (POTENTIAL).
CC DOMAIN 303 352 CYTOPLASMIC (POTENTIAL).
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CC DOMAIN 3381 3410 111 (POTENTIAL).
CC TRANSMEM 3411 3440 112 (POTENTIAL).
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CC DOMAIN 3741 3770 123 (POTENTIAL).
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CC DOMAIN 3801 3830 125 (POTENTIAL).
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CC TRANSMEM 4131 4160 136 (POTENTIAL).
CC DOMAIN 4161 4190 137 (POTENTIAL).
CC TRANSMEM 4191 4220 138 (POTENTIAL).
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CC DOMAIN 4341 4370 143 (POTENTIAL).
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CC DOMAIN 4401 4430 145 (POTENTIAL).
CC TRANSMEM 4431 4460 146 (POTENTIAL).
CC DOMAIN 4461 4490 147 (POTENTIAL).
CC TRANSMEM 4491 4520 148 (POTENTIAL).
CC DOMAIN 4521 4550 149 (POTENTIAL).
CC TRANSMEM 4551 4580 150 (POTENTIAL).
CC DOMAIN 4581 4610 151 (POTENTIAL).
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OC NCBI_TaxID=54180;
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RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075442; AAD19854.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
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FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
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SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 16
ID CCR5_TRAPH STANDARD; PRT; 352 AA.
AC 097879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;

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OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075443; AAD19855.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
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FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
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FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
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Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 17
ID CCR5_MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN CCR5 OR CMKBR5.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 RC STRAIN=129/SVJ; TISSUE=Spleen;
 RX MEDLINE=96205938; PubMed=9631787;
 RA Boring L., Geeling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
 RA Charo I.F.;
 RT "Molecular cloning and functional expression of murine JE (monocyte
 RT chemoattractant protein 1) and murine macrophage inflammatory protein
 RT 1alpha receptors: evidence for two closely linked C-C chemokine
 RT receptors on chromosome 9.";
 RL J. Biol. Chem. 271:7551-7558(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=96278910; PubMed=8662890;
 RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "Cloning and characterization of a novel murine macrophage
 RT inflammatory protein-1 alpha receptor.";
 RL J. Biol. Chem. 271:14445-14451(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola;
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhlmann S.E., Platt E.J., Korak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses.";
 RL J. Virol. 71:8642-8656(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=97404635; PubMed=9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharon M., Cen Y.H.,
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 RT immunodeficiency virus type 1.";
 RL J. Virol. 71:6305-6314(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Guo B., Kuno K., Harada A., Matsushima K.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
 CC but not in nonhematopoietic cell lines.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; U47036; AAC52454.1; -
 CC EMBL; X94151; CAA63857.1; -
 CC EMBL; U68565; AAB37273.1; -
 CC EMBL; U83327; AAC53386.1; -
 CC EMBL; AF022990; AAC53389.1; -
 CC EMBL; AF019772; AAB71183.1; -
 CC EMBL; D83648; BAA12024.1; -
 CC MGD; MG1:107182; Ccr5.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
 DR GO; GO:0006932; P:defense response; IMP.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G PROTEIN RECF F1_1; 1.
 DR PROSITE; PS0262; G PROTEIN RECF F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
 FT DOMAIN 1 32
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 33 60
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 61 70
 FT TRANSMEM 71 91
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 92 104
 FT TRANSMEM 105 126
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 127 143
 FT TRANSMEM 144 168
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 169 200
 FT TRANSMEM 201 220
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 221 237
 FT TRANSMEM 238 262
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 263 279
 FT TRANSMEM 280 303
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 304 354
 FT CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 103 180
 FT DISULFID 270 270
 FT VARIANT 11 11
 FT I -> S.
 FT VARIANT 62 62
 FT K -> R.
 FT VARIANT 66 66
 FT V -> M.
 FT VARIANT 97 97
 FT I -> V.
 FT VARIANT 109 109
 FT V -> L.
 FT VARIANT 156 156
 FT V -> A.
 FT VARIANT 160 160
 FT F -> S.
 FT VARIANT 185 185
 FT P -> L.
 FT VARIANT 213 213
 FT I -> V.
 FT VARIANT 318 318
 FT I -> M.
 FT VARIANT 337 337
 FT V -> A.
 FT CONFLICT 3 3
 FT F -> L (IN REF. 2).
 FT CONFLICT 80 80
 FT L -> F (IN REF. 2).
 FT CONFLICT 145 145
 FT N -> I (IN REF. 5).
 FT CONFLICT 190 190
 FT H -> Y (IN REF. 3).
 FT CONFLICT 208 208
 FT P -> S (IN REF. 1).
 SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;
 Query Match 91.5%; Score 108; DB 1; Length 354;
 Best Local Similarity 95.2%; Pred. No. 1.7e-09;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 PYNIVLLNTTFOEFFGLNCS 22
 Db 252 PYNIVLLNTTFOEFFGLNCS 272
 RESULT 18
 CCR5 RAT STANDARD; PRT; 354 AA.
 ID_CCR5 RAT
 AC 008556;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (MIP-1
 DE alpha receptor).
 GN CCR5 OR CCR5R5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=98334064; PubMed=9670989;
 RA Speleis O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
 RA Berger M., Gebicke-Haerter P.J.;
 RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and

upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
 J. Neurosci. Res. 53:16-28(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98318173; PubMed=9555467;
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
 RA Defebvre C.M., Pennell N.A., Streif W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 RT allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; Y12009; AAC72737.1; -;
 CC EMBL; U77350; AAC03243.1; -;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm.1; 1
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G-PROTEIN RECF F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECF F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 33 60 1 (POTENTIAL).
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 71 91 2 (POTENTIAL).
 FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 105 126 3 (POTENTIAL).
 FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 144 168 4 (POTENTIAL).
 FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 201 220 5 (POTENTIAL).
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 238 262 6 (POTENTIAL).
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 280 303 7 (POTENTIAL).
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 103 180 BY SIMILARITY.
 FT CARBOHYD 270 270 N-LINKED (GLCNAc. . .) (POTENTIAL).
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AAAC868D CRC64;
 Query Match 89.0%; Score 105; DB 1; Length 354;
 Best Local Similarity 90.5%; Pred. No. 5.1e-09;
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTFFQFFGLNCS 22
 DB 252 PYNIVLLNTFFQFFGLNCS 272
 RESULT 19
 CKR2 MACMU STANDARD; PRT; 360 AA.
 ID CKR2 MACMU STANDARD; PRT; 360 AA.
 AC O18753;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN CKR2 OR CMKR2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=O18793-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=O18793-2; Sequence=Not described;
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF013958; AAD11572.1; -;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm.1; 1
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G-PROTEIN RECF F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECF F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 KW ALTERNATIVE SPLICING.
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 43 70 1 (POTENTIAL).
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 81 100 2 (POTENTIAL).
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 115 136 3 (POTENTIAL).
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 154 178 4 (POTENTIAL).
 FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 207 226 5 (POTENTIAL).
 FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 244 268 6 (POTENTIAL).
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 286 303 7 (POTENTIAL).
 FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 14 14 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT MOD RES 26 26 SULFATION (BY SIMILARITY).
 FT DISULFID 113 190 BY SIMILARITY.
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;
 Query Match 87.3%; Score 103; DB 1; Length 360;
 Best Local Similarity 90.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PYNIVLLNTFFQFFGLNCS 21
 DB 258 PYNIVLLNTFFQFFGLNCS 277
 RESULT 20
 CKR2 HUMAN STANDARD; PRT; 374 AA.
 ID CKR2 HUMAN STANDARD; PRT; 374 AA.
 AC P41597;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
 KW PROSITE; PS00262; G PROTEIN RECP F1.2; 1.
 FT G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 56 83 1 (POTENTIAL).
 FT DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 94 114 2 (POTENTIAL).
 FT DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 128 149 3 (POTENTIAL).
 FT DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 167 191 4 (POTENTIAL).
 FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 220 239 5 (POTENTIAL).
 FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 257 281 6 (POTENTIAL).
 FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 299 322 7 (POTENTIAL).
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 FT CONFLICT 39 39 Y -> H (IN REF. 1).
 FT CONFLICT 184 184 A -> G (IN REF. 1).
 FT CONFLICT 264 264 V -> G (IN REF. 1).
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 66.9%; Score 79; DB 1; Length 373;
 Best Local Similarity 70.0%; Pred. No. 6.3e-05;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFFQFFGLNNC 21
 ||||| ||||| :|||
 Db 271 PYNIVLFLTFQESLGSNC 290

RESULT 23
 CKRL_HUMAN
 ID CKRL_HUMAN STANDARD; PRT; 355 AA.
 AC P32246;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
 DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
 DE (RANTES-R) (HML45) (LD78 receptor).
 GN CKR1 OR CMKBR1 OR CMKR1.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=93161416; PubMed=7679328;
 RX Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
 RA "Molecular cloning, functional expression, and signaling
 RT characteristics of a C-C chemokine receptor.";
 RL Cell 72:415-425(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93240122; PubMed=7683036;
 RA Gao J.-L., Kuhn D., Tiffany H.L., McDermott D., Li X., Francke U.,
 RA Murphy P.M.;
 RT "Structure and functional expression of the human macrophage
 RT inflammatory protein 1 alpha/RANTES receptor.";
 RL J. Exp. Med. 177:1421-1427(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Monocytes;
 RA MEDLINE=94092629; PubMed=7505609;
 RA Nomura H., Nielsen B.W., Matsumura K.;
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
 RT leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-

CC beta or MCP-1 and subsequently transduces a signal by increasing
 CC the intracellular calcium ions level. Responsible for affecting
 CC stem cell proliferation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
 CC cells.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; L09230; AAA58408.1; -;
 CC EMBL; L10918; AAA36543.1; -;
 CC EMBL; D10925; BAA01723.1; -;
 CC PIR; A45177; A45177.
 CC Genew; HGNC:1602; CCR1.
 CC MIM; 601159; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004950; F:chemokine receptor activity; TAS.
 CC GO; GO:0007155; P:cell adhesion; TAS.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0006935; P:chemotaxis; TAS.
 CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
 CC GO; GO:0006955; P:immune response; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC GO; GO:0007125; P:invasive growth; TAS.
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
 CC PROSITE; PS00262; G PROTEIN RECP F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 35 60 1 (POTENTIAL).
 FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 65 91 2 (POTENTIAL).
 FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 198 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 FT CONFLICT 337 337 E -> D (IN REF. 3).
 SQ SEQUENCE 355 AA; 41172 MW; B2C100FFED275985 CRC64;

Query Match 47.5%; Score 56; DB 1; Length 355;
 Best Local Similarity 40.0%; Pred. No. 0.24;
 Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFFQFFGLNNC 21
 ||||| :||| :|||
 Db 254 PYNIVLLNTFFQFFGLNNC 273

RESULT 24
 RPOB_PINTH
 ID RPOB_PINTH STANDARD; PRT; 1075 AA.
 AC P41607;
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE DNA-directed RNA polymerase beta chain (EC 2.7.7.6).
 GN RPOB.
 OS Pinus thunbergii (Green pine) (Japanese black pine).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95024047; PubMed=7937893;
 RA Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
 RA Sugura M.;
 RT "Loss of all ndh genes as determined by sequencing the entire
 RT chloroplast genome of the black pine Pinus thunbergii.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798 (1994).
 CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 CC of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA} (N).
 CC -!- SUBUNIT: In chloroplasts, the RNA polymerase is composed of four
 CC subunits: alpha, beta, beta', and beta".
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- SIMILARITY: Belongs to the RNA polymerase beta chain family.
 CC -----
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 CC -----
 CC EMBL: D17510; BAB04326.1; --
 CC PIR: T07448; T07448.
 DR HSSP; Q9KWU7; IJQM.
 DR InterPro: IPR007121; RNA_pol_B.
 DR InterPro: IPR007644; RNA_pol_Rpb2_1.
 DR InterPro: IPR007642; RNA_pol_Rpb2_2.
 DR InterPro: IPR007645; RNA_pol_Rpb2_3.
 DR InterPro: IPR007120; RNA_pol_Rpb2_6.
 DR InterPro: IPR007641; RNA_pol_Rpb2_7.
 DR Pfam: PF04563; RNA_pol_Rpb2_1; 1.
 DR Pfam: PF04561; RNA_pol_Rpb2_2; 1.
 DR Pfam: PF04565; RNA_pol_Rpb2_3; 1.
 DR Pfam: PF00562; RNA_pol_Rpb2_6; 1.
 DR Pfam: PF04560; RNA_pol_Rpb2_7; 1.
 DR PROSITE; PS01166; RNA_POL_BETA; 1.
 DR Transference; DNA-directed RNA polymerase; Transcription; Chloroplast.
 KW SEQUENCE 1075 AA; 122470 MW; 00677BC6D8F26ACA CRC64;
 SQ
 Query Match 46.2%; Score 54.5; DB 1; Length 1075;
 Best Local Similarity 63.2%; Pred. No. 1.2;
 Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1;
 QY 2 PYNIY---LILNTQFFQG 17
 DB 355 PQNLVTSLLKNVQDFG 373

 RESULT 25
 ID_CK4_HUMAN STANDARD; PRT; 360 AA.
 AC P51679; Q9ULY6; Q9ULY7;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4)
 DE (K5-5).
 GN CCR4 OR CMK4.
 OS Homo sapiens (Human).
 CC

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=95370289; PubMed=7642634;
 RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
 RA Proudfoot A.E.I., Wells T.N.C.;
 RT "Molecular cloning and functional expression of a novel CC chemokine
 RT receptor cDNA from a human basophilic cell line.";
 RL J. Biol. Chem. 270:19495-19500 (1995).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
 RX MEDLINE=21040311; PubMed=11196669;
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
 RA Hirai K., Tokunaga K.;
 RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
 RL Genes Immun. 1:97-104 (1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=97313486; PubMed=9169480;
 RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
 RT "The T cell-directed CC chemokine TARC is a highly specific
 RT biological ligand for CC chemokine receptor 4.";
 RL J. Biol. Chem. 272:15036-15042 (1997).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=98104168; PubMed=9430724;
 RA Imai T., Chantray D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
 RA Yoshie O., Gray P.W.;
 RT "Macrophage-derived chemokine is a functional ligand for the CC
 RT chemokine receptor 4.";
 RL J. Biol. Chem. 273:1764-1768 (1998).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=99394604; PubMed=10466728;
 RA Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,
 RA Andrew D.P., Warnke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
 RT "The chemokine receptor CCR4 in vascular recognition by cutaneous but
 RT not intestinal memory T cells.";
 RL Nature 400:776-780 (1999).
 RN [7]
 RP FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
 RX MEDLINE=20219238; PubMed=10754297;
 RA Inggerdingen M., Damaj B., Maghazachi A.A.;
 RT "Human NK cells express CC chemokine receptors 4 and 8 and respond to
 RT thymus and activation-regulated chemokine, macrophage-derived
 RT chemokine, and I-309.";
 RL J. Immunol. 164:4048-4054 (2000).
 CC -!- FUNCTION: High affinity receptor for the C-C type chemokines
 CC TARC/SCYAL7 and MDC/SCYAL22. The activity of this receptor is
 CC mediated by G(i) proteins which activate a phosphatidylinositol-
 CC calcium second messenger system. Can function as a chemoattractant
 CC homing receptor on circulating memory lymphocytes and as a
 CC coreceptor for some primary HIV-2 isolates. In the CNS, could
 CC mediate hippocampal-neuron survival.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in
 CC peripheral blood leukocytes, including T cells, mostly cd4+ cells,
 CC and basophils, and in platelets; at lower levels, in the spleen
 CC and in monocytes. Detected also in macrophages, IL-2-activated
 CC natural killer cells and skin-homing memory T cells, mostly the
 CC ones expressing the cutaneous lymphocyte antigen (CLA). Expressed
 CC in brain microvascular and coronary artery endothelial cells.
 CC -!- PTM: IN NATURAL KILLER CELLS, SCYAL2 BINDING INDUCES
 CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY

FT	DISULFID	106	183	BY SIMILARITY.
FT	VARIANT	218	218	C -> S (polymorphism found in about 7% of the population; may show reduced activity).
FT	FT			/FTID=VAR_010668.
FT	CONFLICT	276	276	S -> T (IN REF. 4 AND 5).
FT	SEQUENCE	355 AA;	41043 MW;	E95DCD7A6C643874 CRC64;
QY	Query Match	44.1%;	Score 52;	DB 1; Length 355;
	Best Local Similarity	40.0%;	Pred. No. 1;	
	Matches	8; Conservative	6; Mismatches	6; Indels 0; Gaps 0;
QY	2	PYNIVLLANTFOEFFGLNLC	21	
Db	254	PTNVAILLSSYSILFGNDC	273	
RESULT 27				
ID	CKR3 RAT	STANDARD;	PRT;	359 AA.
AC	OS4814;	055169;		
DT	30-MAY-2000	(Rel. 39, Created)		
DT	30-MAY-2000	(Rel. 39, last sequence update)		
DT	10-OCT-2003	(Rel. 42, last annotation update)		
DE	C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)			
DE	(CCR3).			
GN	CR3 OR CMKBR3.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
EN	[1]			
RP	SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.			
RC	STRAIN=Wistar; TISSUE=Spleen;			
RC	MEDLINE=98318173; PubMed=9655467;			
RX	Jiang Y., Salazarica M.N., Adhikari S., Xia Y., Feng L.,			
RA	Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.,			
RA	"Chemokine receptor expression in cultured glia and rat experimental			
RT	allergic encephalomyelitis";			
RT	J. Neuroimmunol. 86:1-12(1998).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Wistar; TISSUE=Spleen;			
RC	Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;			
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,			
CC	MCP-3, MCP-4 and RANTES and subsequently transduces a signal by			
CC	increasing the intracellular calcium ions level (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or			
CC	microglia.			
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
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CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announcement/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; AF003954; AAC03337.1; "			
DR	EMBL; Y13400; CAA73830.1; "			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Flam; PF00001; 7tm.1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPSN.			
DR	PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.			
DR	PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.			
KW	G-protein coupled receptor; Transmembrane.			
DOMAIN	1 43 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM	44 64	POTENTIAL.	
FT	DOMAIN	65 74	CYTOSOLIC (POTENTIAL).	
FT	TRANSMEM	75 95	POTENTIAL.	

FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 113 133 POTENTIAL.
 FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 155 175 POTENTIAL.
 FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 207 227 POTENTIAL.
 FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 244 264 POTENTIAL.
 FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 289 309 POTENTIAL.
 FT DOMAIN 310 339 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 164 184 F -> L (IN REF. 2).
 SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;
 Query Match 44.1%; Score 52; DB 1; Length 359;
 Best Local Similarity 50.0%; Pred. No. 1;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 Qy 2 PYNIVLLNTFQFFGLNMC 21
 Db 258 PYNVLLLSAFHSTLETSCT 277
 RESULT 28
 CKR4_MOUSE
 ID CKR4_MOUSE STANDARD; PRT; 360 AA.
 AC P51680;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 4 (C-CR-4) (CCR-4) (CCR4).
 GN CCR4 OR CMKR4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=96136324; PubMed=8573157;
 RA Hoogewerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "Molecular cloning of murine CC CKR-4 and high affinity binding of
 chemokines to murine and human CC CKR-4.";
 RL Biochem. Biophys. Res. Commun. 218:337-343 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;
 RX MEDLINE=97335974; PubMed=9192769;
 RA Yoon B.-S., Kim S.-H., Lyu M.S., Kozak C.A., Taub D.D., Kwon B.S.;
 RT "Molecular cloning and characterization of a cDNA, CHEM1, encoding a
 chemokine receptor with a homology to the human C-C chemokine
 receptor, CCR-4.";
 RL Blood 89:4448-4460 (1997).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20273981; PubMed=10811868;
 RA Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
 RT "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced
 endotoxic shock.";
 RL J. Exp. Med. 191:1755-1764 (2000).
 CC -1- FUNCTION: High affinity receptor for the C-C type chemokines
 TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
 mediated by G(i) proteins which activate a phosphatidylinositol-
 calcium second messenger system. Could play a role in
 lipopolysaccharide (LPS)-induced endotoxic shock. In the CNS,
 could mediate hippocampal-neuron survival.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in the thymus, macrophages and T-
 and B-cells.
 CC -1- DEVELOPMENTAL STAGE: Low expression at 7.5 dpc and 12.5 dpc in the
 yolk sac.
 CC -1- IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
 PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY

CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X90862; CAA62372.1; -;
 DR EMBL; U15208; AAA92582.1; -;
 DR PIR; JC4587; JC4587.
 DR MGD; MGI:107824; Ccr4.
 DR GO; GO:0016493; Fc-C chemokine receptor activity; IMP.
 DR GO; GO:0066935; P:chemotaxis; IMP.
 DR GO; GO:006954; P:inflammatory response; IMP.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PROSITE; PS00237; G PROTEIN RECP Fl.1; 1.
 DR PROSITE; PS50262; G PROTEIN RECP Fl.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Phosphorylation.
 KW DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 40 67 1 (POTENTIAL).
 FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 78 98 2 (POTENTIAL).
 FT DOMAIN 99 111 3 (POTENTIAL).
 FT TRANSMEM 112 133 3 (POTENTIAL).
 FT DOMAIN 134 150 4 (POTENTIAL).
 FT TRANSMEM 151 175 5 (POTENTIAL).
 FT DOMAIN 176 206 5 (POTENTIAL).
 FT TRANSMEM 207 226 6 (POTENTIAL).
 FT DOMAIN 227 242 7 (POTENTIAL).
 FT TRANSMEM 243 267 7 (POTENTIAL).
 FT DOMAIN 268 284 7 (POTENTIAL).
 FT TRANSMEM 285 308 7 (POTENTIAL).
 FT DOMAIN 309 360 7 (POTENTIAL).
 FT TRANSMEM 343 346 POLY-SER.
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT DISULFID 110 187 BY SIMILARITY.
 FT CONFLICT 4 4 T -> I (IN REF. 2).
 FT CONFLICT 145 145 S -> T (IN REF. 2).
 FT CONFLICT 181 181 E -> Q (IN REF. 2).
 FT CONFLICT 205 205 E -> D (IN REF. 2).
 FT CONFLICT 221 221 W -> C (IN REF. 2).
 FT CONFLICT 241 241 V -> L (IN REF. 2).
 FT CONFLICT 246 246 G -> A (IN REF. 2).
 FT CONFLICT 293 293 G -> A (IN REF. 2).
 FT CONFLICT 311 311 F -> S (IN REF. 2).
 SQ SEQUENCE 360 AA; 41462 MW; 97BDB8C96D259AE3 CRC64;
 Query Match 44.1%; Score 52; DB 1; Length 360;
 Best Local Similarity 47.6%; Pred. No. 1;
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 Qy 2 PYNIVLLNTFQFFGLNMC 22
 Db 257 PYNVLFLETLVEVLQDCT 277
 RESULT 29
 ACM2_PANTR
 ID ACM2_PANTR STANDARD; PRT; 440 AA.
 AC Q9N2A7;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Muscarinic acetylcholine receptor M2 (Fragment).


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CHRM2.
GN Pan troglodytes (Chimpanzee).
OS
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OC NCBI_TaxID=9598;
OX
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 220.
RC Kitano T., Kobayakawa H., Saitou N.;
RT "Silver project.";
RT
RL SUBMITTED (APR-2000) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS.
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
CC ADENYLATE CYCLASE INHIBITION.
CC
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
-----
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CC
-----
CC EMBL; AB041392; BAA94477.1; -.
CC InterPro; IPR000276; GPCR_Rhodpan.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; GPCRHOOPS.
CC PROSITE; PS0263; G PROTEIN RECF F1.1; 1.
CC PROSITE; PS0263; G PROTEIN RECF F1.2; 1.
CC KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
CC Phosphorylation; Multigene family; G-protein coupled receptor.
CC
CC NON_FER 1 1
CC TRANSFAM <1 19 1 (POTENTIAL).
CC DOMAIN 20 33 CYTOPLASMIC (POTENTIAL).
CC TRANSFAM 34 54 2 (POTENTIAL).
CC DOMAIN 55 71 EXTRACELLULAR (POTENTIAL).
CC TRANSFAM 72 93 3 (POTENTIAL).
CC DOMAIN 94 113 CYTOPLASMIC (POTENTIAL).
CC TRANSFAM 114 136 4 (POTENTIAL).
CC DOMAIN 137 158 EXTRACELLULAR (POTENTIAL).
CC TRANSFAM 159 181 5 (POTENTIAL).
CC DOMAIN 182 362 CYTOPLASMIC (POTENTIAL).
CC TRANSFAM 363 383 6 (POTENTIAL).
CC DOMAIN 384 397 EXTRACELLULAR (POTENTIAL).
CC TRANSFAM 398 417 7 (POTENTIAL).
CC DOMAIN 418 440 CYTOPLASMIC (POTENTIAL).
CC TRANSFAM 470 150 BY SIMILARITY.
CC DISULFID 70 420 PHOSPHORYLATION (POTENTIAL).
CC MOD_RES 420 420 PHOSPHORYLATION (POTENTIAL).
CC MOD_RES 424 424 PHOSPHORYLATION (POTENTIAL).
CC MOD_RES 439 439 PHOSPHORYLATION (POTENTIAL).
CC SEQUENCE 440 AA; 48854 MW; 12B0324E13D37DDF CRC64;
CC
Query Match 44.1%; Score 52; DB 1; Length 440;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVILLNTFF 12
||||:|||||
Db 375 APYNVVLLNTFF 386
-----
RESULT 30
ID ACW2 HUMAN STANDARD; PRT; 466 AA.
ID ACW2 HUMAN
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Muscarinic acetylcholine receptor M2.

```

FT TRANSMEM	23	45	1 (POTENTIAL).
FT DOMAIN	46	59	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	60	80	2 (POTENTIAL).
FT DOMAIN	81	97	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	98	119	3 (POTENTIAL).
FT DOMAIN	120	139	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	140	162	4 (POTENTIAL).
FT DOMAIN	163	184	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	185	207	5 (POTENTIAL).
FT DOMAIN	208	388	CYTOPLASMIC (POTENTIAL).
FT TRANSMEM	389	409	6 (POTENTIAL).
FT DOMAIN	410	423	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	424	443	7 (POTENTIAL).
FT DOMAIN	444	466	CYTOPLASMIC (POTENTIAL).
FT CARBOHYD	2	2	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	3	3	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	6	6	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	9	9	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID	96	176	BY SIMILARITY.
FT MOD_RES	446	446	PHOSPHORYLATION (POTENTIAL).
FT MOD_RES	450	450	PHOSPHORYLATION (POTENTIAL).
FT MOD_RES	465	465	PHOSPHORYLATION (POTENTIAL).
SQ SEQUENCE	466 AA;	51715 MW;	2FC2FD7748C22BEC CRC64;

Query Match 44.1%; Score 52; DB 1; Length 466;
 Best Local Similarity 66.7%; Pred. No. 1.3;
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTF 12
 |||:::|
 Db 401 APYNVLLNTF 412

Search completed: March 4, 2004, 18:00:07
 Job time : 8.38367 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 35.4694 Seconds
(without alignments)
195.701 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APNVILLNTTQEPFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query #			DB ID	Description
	Score	Match	Length		
SUMMARIES					
1	118	100.0	333	4	O14694
2	118	100.0	334	6	Q9TUQ7
3	118	100.0	339	4	Q9UN24
4	118	100.0	339	4	Q9UN26
5	118	100.0	339	4	Q9UN23
6	118	100.0	339	4	Q9UBJ7
7	118	100.0	339	4	Q9UN25
8	118	100.0	339	4	Q9UN27
9	118	100.0	339	4	Q9UBT9
10	118	100.0	339	6	Q9TQM0
11	118	100.0	339	6	Q9TUX1
12	118	100.0	339	6	Q9TUN9
13	118	100.0	339	6	Q9TUN8
14	118	100.0	339	6	Q9TUT4
15	118	100.0	339	6	Q9TUM9
16	118	100.0	339	6	Q9TSQL
					O14694
					Q9TUQ7
					Q9UN24
					Q9UN26
					Q9UN23
					Q9UBJ7
					Q9UN25
					Q9UN27
					Q9UBT9
					Q9TQM0
					Q9TUX1
					Q9TUN9
					Q9TUN8
					Q9TUT4
					Q9TUM9
					Q9TSQL
					hylobates c
					erythrocebu
					macaca nemo
					hylobates c
					ceropithes

Q8TUN8 cercopithec
Q8TQW4 pan troglod
Q8TUN4 pan troglod
Q8TQW7 cercopithec
Q8TQW5 erythrocebu
Q8TUN9 saguinus sp
Q8TQW0 macaca fasc
Q8TUN9 macaca mula
Q8TUN2 macaca fasc
Q8TUN6 cercopithec
Q8TQW6 colobus gue
Q8TUN9 cercopithec
Q8TUN3 macaca fasc
Q8TUN7 macaca fusc
Q8TUN0 macaca mula
Q8TQW2 papio papio
Q8TUN5 cercopithec
Q8TUN7 papio papio
Q8TUN7 pan troglod
Q8TUN3 pongo pygma
Q8TUN5 papio papio
Q8TUN0 macaca mula
Q8TQW2 papio papio
Q8TQW3 cercopithec
Q8TUN8 cercopithec
Q8TUN3 erythrocebu
Q8TQW2 pongo pygma
Q8TUN1 macaca mula
Q8TUN6 macaca neme
Q8TQW2 erythrocebu
Q8TUN4 mandrillus
Q8TQW3 mandrillus
Q8TQW4 cercopithec
Q8TUN0 macaca neme
Q8TQW2 gorilla gor
Q8TUN8 macaca mula
Q8TUN1 macaca neme
Q8TQW3 cercopithec
Q8TUN5 pan troglod
Q8TUN4 erythrocebu
Q8TQW6 erythrocebu
Q8TQW2 macaca neme
Q8TQW1 macaca mula
Q8TUN5 macaca neme
Q8TUN2 macaca neme
Q8TUN8 papio papio
Q8TUN4 macaca mula
Q8TUN6 papio papio
Q8TQW4 cercopithec
Q8TQW6 cercopithec
Q8TUN7 macaca mula
Q8TUN0 hylobates c
Q8TQW2 cercopithec
Q8TUN8 cercopithec
Q8TUN1 cercopithec
Q8TUN9 papio papio
Q8TUN2 macaca mula
Q8TUN8 cercocebu
Q8TQW3 cercocebu
Q8TQW5 hylobates s
Q8TUN5 hylobates s
Q8TUN4 cercopithec
Q8TUN9 cercocebu
Q8TUN14 colobus gue
Q8TQW6 cercopithec
Q8TUN3 miopithecus
Q8TQW1 pan troglod
Q8TUN7 cercopithec
Q8TUN4 theropithec
Q8TUN1 theropithec
Q8TUN6 trachypithe
Q8TUN8 colobus pol
Q8TUN4 cercopithec

90 118 100.0 352 6 Q95NC7
 91 118 100.0 352 6 Q95NC0
 92 118 100.0 352 6 Q95GN5
 93 118 100.0 352 6 Q97975
 94 118 100.0 352 6 Q9XT12
 95 118 100.0 352 6 Q9XS35
 96 118 100.0 352 6 Q9TV42
 97 118 100.0 352 6 Q9XT13
 98 118 100.0 352 6 Q95ND2
 99 118 100.0 352 6 Q97776
 100 118 100.0 352 6 Q9TV93

ALIGNMENTS

RESULT 1
 O14694
 ID O14694 PRELIMINARY; PRT; 333 AA.
 AC O14694;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE CCR5 receptor (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
 DR EMBL; AF011504; AAB65704.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 FT NON TER 333 333
 FT SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;
 SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 118; DB 4; Length 333;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYVILLNTFQFFGLNCS 22
 DB 230 APYVILLNTFQFFGLNCS 251

RESULT 2
 Q9TUQ7
 ID Q9TUQ7 PRELIMINARY; PRT; 334 AA.
 AC Q9TUQ7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Erythrocybus patas (Red guenon) (Hussar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Erythrocybus.
 OX NCBI_TaxID=9538;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RA "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162049; AAD47804.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 FT NON TER 334 334
 FT SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;
 SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 334;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYVILLNTFQFFGLNCS 22
 DB 237 APYVILLNTFQFFGLNCS 258

RESULT 3
 Q9UN24
 ID Q9UN24 PRELIMINARY; PRT; 339 AA.
 AC Q9UN24;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RA "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161919; AAD47676.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 FT NON TER 339 339
 FT SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;
 SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 APYVILLNTFQFFGLNCS 22
 DB 242 APYVILLNTFQFFGLNCS 263

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RESULT 4
Q9UN26
ID Q9UN26 PRELIMINARY; PRT; 339 AA.
AC Q9UN26;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161916; AAD47673.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLNTFOEFFGLNCS 22
|||||
DB 242 APYIVLLNTFOEFFGLNCS 263

RESULT 5
Q9UN23
ID Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLNTFOEFFGLNCS 22
|||||
DB 242 APYIVLLNTFOEFFGLNCS 263

RESULT 6
Q9UBJ7
ID Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FF1F2F27A CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLNTFOEFFGLNCS 22
|||||
DB 242 APYIVLLNTFOEFFGLNCS 263

RESULT 7
Q9UN25
ID Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161918; AAD47675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQFFGLNCS 22
|||||
DB 242 APYNIIVLLNTFQFFGLNCS 263

RESULT 8
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQFFGLNCS 22
|||||
DB 242 APYNIIVLLNTFQFFGLNCS 263

RESULT 9
Q9UBT9
ID Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQFFGLNCS 22
|||||
DB 242 APYNIIVLLNTFQFFGLNCS 263

RESULT 10
Q9TQW0
ID Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.

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DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 00007186; P: G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G PROTEIN RECF F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTQFEFFGLNCS 22
DB 242 APYNIIVLLNTQFEFFGLNCS 263

RESULT 11
Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 00007186; P: G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G PROTEIN RECF F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257F8B834C4AE CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTQFEFFGLNCS 22
DB 242 APYNIIVLLNTQFEFFGLNCS 263

RESULT 12
Q9TUU9 PRELIMINARY; PRT; 339 AA.
AC Q9TUU9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161948; AAD47704.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 00007186; P: G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G PROTEIN RECF F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTQFEFFGLNCS 22
DB 242 APYNIIVLLNTQFEFFGLNCS 263

RESULT 13
Q9TUW8 PRELIMINARY; PRT; 339 AA.
AC Q9TUW8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 00007186; P: G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G PROTEIN RECF F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

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Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 14
Q9TUT4
ID Q9TUT4 PRELIMINARY; PRT; 339 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; RAD47734.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 339
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 15
Q9TUT9
ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; RAD47734.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 339
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 16
Q9TSQ1
ID Q9TSQ1 PRELIMINARY; PRT; 339 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; RAD47778.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 339
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39216 MW; 847E935FA403E52D CRC64;

Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 17
Q9TU08
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species";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; RAD47647.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 339
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match      100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
   |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 17
Q9TU08
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ID QPTU08 PRELIMINARY; PRT; 339 AA.
AC QPTU08;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 242 APYNIVLLNTFOEFFGLNCS 263

RESULT 18
QPTQW4
ID QPTQW4 PRELIMINARY; PRT; 339 AA.
AC QPTQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 242 APYNIVLLNTFOEFFGLNCS 263

RESULT 18
QPTQW4
ID QPTQW4 PRELIMINARY; PRT; 339 AA.
AC QPTQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8B8601D46A4 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 242 APYNIVLLNTFOEFFGLNCS 263

RESULT 19
QPTUW4
ID QPTUW4 PRELIMINARY; PRT; 339 AA.
AC QPTUW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39159 MW; 85699E882BAC0E84 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 242 APYNIVLLNTFOEFFGLNCS 263

RESULT 20
QPTQV7
ID QPTQV7 PRELIMINARY; PRT; 339 AA.
AC QPTQV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

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OC Cercopithecinae; Cercopithecus.
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92B03E62 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
DB 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 21
Q9TUQ5 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162054; AAD47809.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39048 MW; 1A2EL9E3A6A5A52A CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
DB 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 22
Q9TUR9 PRELIMINARY; PRT; 339 AA.
AC Q9TUR9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saginus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD47770.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
DB 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 23
Q9TQT0 PRELIMINARY; PRT; 339 AA.
AC Q9TQT0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD47710.1; -.

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DR EMBL; AF161950; AAD47706.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 24
Q9TUN9
ID Q9TUN9 PRELIMINARY; PRT; 339 AA.
AC Q9TUN9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161972; AAD47727.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCB5BA96C2F98 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 25
Q9TSN2
ID Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.

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AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47709.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39137 MW; 9E626ED3288607C1 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
Db 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 26
Q9TUR6
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.

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KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQFFFGLNCS 22
DB 242 APYNVILLNTQFFFGLNCS 263

RESULT 27
Q9TQV6 PRELIMINARY; PRT; 339 AA.
AC Q9TQV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47756.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72F8F566F CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQFFFGLNCS 22
DB 242 APYNVILLNTQFFFGLNCS 263

RESULT 28
Q9TQV6 PRELIMINARY; PRT; 339 AA.
AC Q9TQV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.

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OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercopithecus.
OX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162041; AAD47796.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF1F3ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQFFFGLNCS 22
DB 242 APYNVILLNTQFFFGLNCS 263

RESULT 29
Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161951; AAD47707.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39098 MW; F0132E8BC44EF829 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;

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Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
|||||
DB 242 APYNIVLLNTFQEFFGLNCS 263

RESULT 30

Q9TUU7
ID Q9TUU7 PRELIMINARY; PRT; 339 AA.
AC Q9TUU7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprea J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161955; AA04711.1; --
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22
|||||
DB 242 APYNIVLLNTFQEFFGLNCS 263

Search completed: March 4, 2004, 18:02:56
Job time : 36.4694 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	118	100.0	352	3	US-08-466-343D-13	Sequence 2, Appli
2	118	100.0	352	3	US-09-087-232A-13	Sequence 13, Appl
3	118	100.0	352	3	US-08-861-105-14	Sequence 14, Appl
4	118	100.0	352	3	US-08-575-967A-2	Sequence 2, Appli
5	118	100.0	352	3	US-09-045-583-52	Sequence 52, Appl
6	118	100.0	352	4	US-09-517-605-5	Sequence 5, Appli
7	118	100.0	352	4	US-09-534-185-52	Sequence 52, Appl
8	118	100.0	352	4	US-08-833-752-5	Sequence 5, Appli
9	118	100.0	352	4	US-09-502-783A-2	Sequence 2, Appli
10	118	100.0	352	4	US-09-796-202-1	Sequence 1, Appli
11	108	91.5	354	4	US-08-724-984A-2	Sequence 2, Appli
12	103	87.3	329	4	US-09-502-783A-9	Sequence 8, Appli
13	103	87.3	344	3	US-08-466-343D-9	Sequence 9, Appli
14	103	87.3	347	1	US-08-461-244-3	Sequence 3, Appli
15	103	87.3	360	1	US-08-450-393A-4	Sequence 4, Appli
16	103	87.3	360	3	US-08-446-669-4	Sequence 4, Appli
17	103	87.3	360	3	US-09-045-583-50	Sequence 50, Appl
18	103	87.3	360	3	US-09-045-583-51	Sequence 51, Appl
19	103	87.3	360	4	US-09-534-185-50	Sequence 50, Appl
20	103	87.3	360	4	US-09-534-185-51	Sequence 51, Appl
21	103	87.3	360	4	US-08-833-752-7	Sequence 7, Appli
22	103	87.3	360	4	US-09-131-827A-2	Sequence 2, Appli
23	103	87.3	360	4	US-09-131-827A-20	Sequence 20, Appl
24	103	87.3	360	5	UCT-US95-00476-4	Sequence 4, Appli
25	103	87.3	374	1	US-08-450-393A-2	Sequence 2, Appli
26	103	87.3	374	3	US-08-446-669-2	Sequence 2, Appli
27	103	87.3	374	5	UCT-US95-00476-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
 US-08-466-343D-2
 ; Sequence 2, Application US/08466343D
 ; Patent No. 6025154
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, YI
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
 ; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVE., NW, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/466,343D
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEFFE, ERIC K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-466-343D-2

Query Match 100.0%; Score 118; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.1e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTLTFQFFGLNCS 22
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 Db 249 APYNVLLNTLTFQFFGLNCS 270

RESULT 2
 US-09-087-232A-13
 ; Sequence 13, Application US/09087232A
 ; Patent No. 6153431
 ; GENERAL INFORMATION:
 ; APPLICANT: Quillent et al.
 ; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
 ; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
 ; STREET: 30 Rockefeller Plaza
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10112
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/087,232A
 ; FILING DATE: 28 MAY 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/049,057
 ; FILING DATE: 30 MAY 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOLE, LISA B.
 ; REGISTRATION NUMBER: 35,225
 ; REFERENCE/DOCKET NUMBER: AP 31115
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 408-2628
 ; TELEFAX: (212) 765-2519
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-087-232A-13

Query Match 100.0%; Score 118; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 4.1e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTLTFQFFGLNCS 22
 |||||
 Db 249 APYNVLLNTLTFQFFGLNCS 270

RESULT 3
 US-08-861-105-14
 ; Sequence 14, Application US/08861105
 ; Patent No. 6258527
 ; GENERAL INFORMATION:
 ; APPLICANT: LITTMAN, DAN R.
 ; APPLICANT: DENG, HONGKUI
 ; APPLICANT: ELMMEIER, WILFRIED
 ; APPLICANT: LANDAU, NATHANIEL R.
 ; APPLICANT: LIU, RONG
 ; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
 ; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; STREET: Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/861,105
 ; FILING DATE:
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/666,020
 ; FILING DATE: 19-JUN-1996
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/227,319
 ; FILING DATE: 13-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-861-105-14

Query Match 100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 4
US-08-575-967A-2
Sequence 2, Application US/0857967A
Patent No. 6265184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: /= "88C amino acid sequence"
US-08-575-967A-2

Query Match 100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22

DB 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 5
US-09-045-583-52
Sequence 52, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-WAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-52

Query Match 100.0%; Score 118; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
DB 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 6
US-09-517-605-5
Sequence 5, Application US/09517605
Patent No. 6391567
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
CELLS
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5


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; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-5

Query Match      100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APYNIVLLILNTFOEFGLNCS 22
        |||||
        249 APYNIVLLILNTFOEFGLNCS 270
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RESULT 7
US-03-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: NO. 6403767el Molecules of the G Protein-Coupled
; Heptahelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; HARDWARE: Bareit in Release #1.0
; Version #1.25

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/534,185
  FILING DATE: 24-Mar-2000
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/045,583
  FILING DATE: <Unknown>

```

NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: WNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

DB 249 APYNVLLNTFQEFFGLNCS 270

RESULT 8
US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375

SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-343D-9

Query Match 87.3%; Score 103; DB 3; Length 344;
Best Local Similarity 90.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFQEFFGLNLC 21
DB 241 PYNIVLLNTFQEFFGLSNC 260

RESULT 14
US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-3

Query Match 87.3%; Score 103; DB 1; Length 347;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFQEFFGLNLC 21
DB 245 PYNIVLLNTFQEFFGLSNC 264

RESULT 15
US-08-450-393A-4
; Sequence 4, Application US/08450393A

Patent No. 5707815
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMAOTTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,393A
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELEPHONE: 415-843-5165
TELEFAX: 415-8857-0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 87.3%; Score 103; DB 1; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFQEFFGLNLC 21
DB 258 PYNIVLLNTFQEFFGLSNC 277

RESULT 16
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMAOTTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,669
FILING DATE: May 25, 1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-4

Query Match 87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFFGLNNC 21
Db 258 PYNIVLLNTQEFFGLSNC 277

RESULT 17
US-09-045-583-50
Sequence 50, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-50

Query Match 87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFFGLNNC 21
Db 258 PYNIVLLNTQEFFGLSNC 277

RESULT 18

US-09-045-583-51
Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-51

Query Match 87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFFGLNNC 21
Db 258 PYNIVLLNTQEFFGLSNC 277

RESULT 19

US-09-534-185-50
Sequence 50, Application US/09534185
Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)742-4214
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-50

Query Match 87.3%; Score 103; DB 3; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/534,185
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
;
; US-09-534-185-50
;
Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTFOEFFGLNNC 21
Db      258 PYNIVLLNTFOEFFGLSNC 277

RESULT 20
US-09-534-185-51
; Sequence 51, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
;                   Heptahelical Receptor Superfamily and Uses
;                   Therefor
;
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
;
; US-09-534-185-51
;
Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTFOEFFGLNNC 21
Db      258 PYNIVLLNTFOEFFGLSNC 277

RESULT 21
US-08-833-752-7
; Sequence 7, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
;
; US-08-833-752-7
;
Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTFOEFFGLNNC 21
Db      258 PYNIVLLNTFOEFFGLSNC 277

RESULT 22
US-09-131-827A-2
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;
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
;
; US-09-534-185-51
;
Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTFOEFFGLNNC 21
Db      258 PYNIVLLNTFOEFFGLSNC 277

RESULT 21
US-08-833-752-7
; Sequence 7, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
;
; US-08-833-752-7
;
Query Match      87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 PYNIVLLNTFOEFFGLNNC 21
Db      258 PYNIVLLNTFOEFFGLSNC 277

RESULT 22
US-09-131-827A-2
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; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; FILE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-131-827A-2

Query Match 87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 PYNIVLLNTQEFFGLNLC 21
DB 258 PYNIVLLNTQEFFGLSNC 277

RESULT 23
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; FILE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-131-827A-20

Query Match 87.3%; Score 103; DB 4; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 PYNIVLLNTQEFFGLNLC 21
DB 258 PYNIVLLNTQEFFGLSNC 277

RESULT 24
PCT-US95-00476-4
; Sequence 4, Application PC/TUS9500476
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; FILE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 N. Figueroa Street, 5th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00476
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-977-1001
; TELEFAX: 310-977-1003
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-00476-4

Query Match 87.3%; Score 103; DB 5; Length 360;
Best Local Similarity 90.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFFGLNLC 21
DB 258 PYNIVLLNTQEFFGLSNC 277

RESULT 25
US-08-450-393A-2
; Sequence 2, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; FILE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A
; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luanu
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663

APPLICANT: The Regents of the University of California
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Robbins, Berliner & Carson
 STREET: 201 N. Figueroa Street, 5th Floor
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90012-2628
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/00476
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berliner, Robert
 REGISTRATION NUMBER: 20,121
 REFERENCE/DOCKET NUMBER: 5555-291
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-977-1001
 TELEFAX: 310-977-1003
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-00476-2

Query Match 87.3%; Score 103; DB 5; Length 374;
 Best Local Similarity 90.0%; Pred. No. 1.6e-09;
 Matches 18; Conservative 2; Mismatches 0; Indels 0;

QY 2 PYNIVLLNTFQEFFGLSNC 21
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 DB 258 PYNIVLLNTFQEFFGLSNC 277

RESULT 28
 US-08-681-192-2
 ; Sequence 2, Application US/08681192
 ; Patent No. 6287801
 ; GENERAL INFORMATION:
 ; APPLICANT: BERGSM, DEREK
 ; APPLICANT: ELSHOURBAGY, NABIL
 ; APPLICANT: SARAU, HENRY
 ; APPLICANT: RUBEN, STEVEN
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFD5707
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-2799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/681,192
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:

APPLICANT: The Regents of the University of California
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Robbins, Berliner & Carson
 STREET: 201 N. Figueroa Street, 5th Floor
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90012-2628
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/00476
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Berliner, Robert
 REGISTRATION NUMBER: 20,121
 REFERENCE/DOCKET NUMBER: 5555-291
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-977-1001
 TELEFAX: 310-977-1003
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 374 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-00476-2

Query Match 87.3%; Score 103; DB 3; Length 374;
 Best Local Similarity 90.0%; Pred. No. 1.6e-09;
 Matches 18; Conservative 2; Mismatches 0; Indels 0;

QY 2 PYNIVLLNTFQEFFGLSNC 21
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 DB 258 PYNIVLLNTFQEFFGLSNC 277

RESULT 27
 PCT-US95-00476-2
 ; Sequence 2, Application PC/TU959500476

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATC50014
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-681-192-2
;
Query Match 59.3%; Score 70; DB 3; Length 344;
Best Local Similarity 57.1%; Pred. No. 0.00063;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQEFFGLNMC 21
Db 252 APYNTAFELSTFKHFSLSDC 272

RESULT 29
US-09-087-232A-22
; Sequence 22, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-087-232A-22
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Query Match 51.7%; Score 61; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTF 12
Db 14 APYNIIVLLNTF 25

RESULT 30
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-012-988A-2
;
Query Match 47.5%; Score 56; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIIVLLNTFQEFFGLNMC 21
Db 254 PYNIIVLLNTFQEFFGLNMC 273

Search completed: March 4, 2004, 18:05:15
Job time : 15.1429 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 18:03:03 ; Search time 29,4082 Seconds
(without alignments)
157.962 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYVILLNTFFQFFGLNCS 22

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Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	118	100.0	332	14	US-10-095-876A-2
3	118	100.0	352	9	US-09-725-285-2
4	118	100.0	352	9	US-09-759-841-2
5	118	100.0	352	9	US-09-779-879A-2
6	118	100.0	352	9	US-09-779-879A-22
7	118	100.0	352	9	US-09-779-880A-2
8	118	100.0	352	9	US-09-779-880A-22
9	118	100.0	352	9	US-09-813-653-15
10	118	100.0	352	9	US-09-813-653-17
11	118	100.0	352	9	US-09-796-202-1
12	118	100.0	352	9	US-09-195-662A-2
13	118	100.0	352	9	US-09-339-912A-2
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18	118	100.0	352	10	US-09-734-221A-14	Sequence 14, Appli
19	118	100.0	352	11	US-09-826-509-477	Sequence 477, App
20	118	100.0	352	13	US-10-106-623-2	Sequence 2, Appli
21	118	100.0	352	13	US-10-106-623-20	Sequence 20, Appli
22	118	100.0	352	14	US-10-232-686-2	Sequence 2, Appli
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24	118	100.0	352	14	US-10-067-800-2	Sequence 2, Appli
25	118	100.0	352	14	US-10-067-800-22	Sequence 22, Appli
26	118	100.0	352	14	US-10-290-058A-6	Sequence 6, Appli
27	118	100.0	352	14	US-10-225-567A-352	Sequence 352, App
28	118	100.0	352	14	US-10-323-314-1	Sequence 1, Appli
29	118	100.0	352	14	US-10-072-301-1	Sequence 1, Appli
30	118	100.0	352	14	US-10-164-649-52	Sequence 52, Appli
31	118	100.0	352	14	US-10-071-866-1	Sequence 1, Appli
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33	118	100.0	352	14	US-10-135-839-22	Sequence 22, Appli
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36	118	100.0	352	14	US-10-439-845-4	Sequence 4, Appli
37	118	100.0	352	15	US-10-360-828-1	Sequence 1, Appli
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41	103	87.3	329	9	US-09-502-783A-9	Sequence 9, Appli
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47	103	87.3	347	9	US-09-104-792-3	Sequence 3, Appli
48	103	87.3	347	14	US-10-176-078-3	Sequence 2, Appli
49	103	87.3	360	9	US-09-131-827A-2	Sequence 20, Appli
50	103	87.3	360	9	US-09-131-827A-20	Sequence 7, Appli
51	103	87.3	360	9	US-09-938-719-7	Sequence 7, Appli
52	103	87.3	360	9	US-09-939-226-7	Sequence 7, Appli
53	103	87.3	360	11	US-09-938-703-7	Sequence 7, Appli
54	103	87.3	360	11	US-09-826-509-473	Sequence 473, App
55	103	87.3	360	14	US-10-225-567A-460	Sequence 460, App
56	103	87.3	360	14	US-10-164-649-50	Sequence 50, Appli
57	103	87.3	360	14	US-10-164-649-51	Sequence 51, Appli
58	103	87.3	360	14	US-10-239-423-64	Sequence 64, Appli
59	103	87.3	360	14	US-10-439-845-8	Sequence 8, Appli
60	103	87.3	374	14	US-10-239-423-63	Sequence 63, Appli
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74	70	59.3	344	14	US-10-095-876A-4	Sequence 4, Appli
75	70	59.3	344	14	US-10-223-081-16	Sequence 16, Appli
76	70	59.3	344	14	US-10-223-082-16	Sequence 16, Appli
77	70	59.3	348	14	US-10-029-386-32996	Sequence 32996, A
78	63	53.4	15	10	US-09-805-375-5	Sequence 5, Appli
79	57	48.3	16	14	US-10-439-845-7	Sequence 7, Appli
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81	57	48.3	17	14	US-10-072-301-2	Sequence 2, Appli
82	57	48.3	17	14	US-10-071-866-2	Sequence 2, Appli
83	57	48.3	17	15	US-10-360-828-2	Sequence 2, Appli
84	57	48.3	17	15	US-10-371-483-4	Sequence 4, Appli
85	57	48.3	17	14	US-10-084-813-96	Sequence 96, Appli
86	57	48.3	138	14	US-10-057-890A-10	Sequence 10, Appli
87	57	48.3	157	14	US-10-057-890A-31	Sequence 31, Appli
88	56	47.5	209	9	US-09-925-302-752	Sequence 752, App

Sequence 58, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 62, Appl
Sequence 2, Appl
Sequence 14, Appl
Sequence 62, Appl
Sequence 9, Appl
Sequence 2, Appl
Sequence 78, Appl
Sequence 8, Appl
Sequence 8, Appl

89 56 47.5 279 15 US-10-174-364-58
90 56 47.5 355 9 US-09-961-068-1
91 56 47.5 355 9 US-09-960-547-1
92 56 47.5 355 14 US-10-225-567A-62
93 56 47.5 355 14 US-10-245-850-2
94 56 47.5 355 14 US-10-376-564-14
95 56 47.5 355 14 US-10-239-423-62
96 56 47.5 355 14 US-10-439-845-9
97 56 47.5 355 15 US-10-452-015-2
98 56 47.5 375 14 US-10-219-834-78
99 55 46.6 355 9 US-09-938-719-8
100 55 46.6 355 9 US-09-939-226-8

ALIGNMENTS

RESULT 1
US-10-084-813-14
; Sequence 14, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-14

Query Match 100.0%; Score 118; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 6e-12; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFGGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 1 APYNVLLNTFOEFGGLNCS 22

RESULT 2
US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030148294A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Bandman, Olga
; APPLICANT: Coleman, Roger; Wilde, Craig G.
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
; FILE REFERENCE: PP-0060-1 CON
; CURRENT APPLICATION NUMBER: US/10/095,876A
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 08/638,081
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861

US-10-095-876A-2

Query Match 100.0%; Score 118; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.1e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFGGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 229 APYNVLLNTFOEFGGLNCS 250

RESULT 3
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR FILING DATE: 09/339,912
; PRIOR APPLICATION NUMBER: 1999-06-25
; PRIOR FILING DATE: 09/195,662
; PRIOR APPLICATION NUMBER: 1998-11-18
; PRIOR FILING DATE: 08/466,343
; PRIOR APPLICATION NUMBER: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFGGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 249 APYNVLLNTFOEFGGLNCS 270

RESULT 4
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manousos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US-09-759-841-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 5

US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 6

US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 7

US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 8

US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match 100.0%; Score 118; DB 9; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVLLNTFQEFFGLNCS 22
DB 249 APYNVLLNTFQEFFGLNCS 270

RESULT 9
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVLLNTFQEFFGLNCS 22
DB 249 APYNVLLNTFQEFFGLNCS 270

RESULT 10
US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVLLNTFQEFFGLNCS 22
DB 249 APYNVLLNTFQEFFGLNCS 270

RESULT 11
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020059813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVLLNTFQEFFGLNCS 22
DB 249 APYNVLLNTFQEFFGLNCS 270

RESULT 12
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNVLLNTFQEFFGLNCS 22
DB 249 APYNVLLNTFQEFFGLNCS 270

RESULT 13
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi

APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNE10
(CCR5 Receptor)
FILE REFERENCE: 1488.1150003
CURRENT APPLICATION NUMBER: US/09/339,912A
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence: Genomic
FEATURE:
OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
|||
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 14
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,719
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 27-JULY-2000
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNIVLLNTFQFFGLNCS 22
|||
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 15
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,226
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
|||
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 16
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kacbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,703
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/626,939
FILING DATE: 2000-07-27
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
|||||
Db 249 APYNVLLNTFQFFGLNCS 270

RESULT 17
US-09-502-783A-2
Sequence 2, Application US/09502783A
Patent No. US20020132269A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
FILE REFERENCE: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
|||||
Db 249 APYNVLLNTFQFFGLNCS 270

RESULT 18
US-09-734-221A-14
Sequence 14, Application US/09734221A
Publication No. US20030096221A1
GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
DENG, HONGKUI
ELMEIER, WILFRIED
LANDAU, NATHANIEL R.
LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/734,221A
FILING DATE: 11-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-004 N2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14
Query Match 100.0%; Score 118; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
|||||
Db 249 APYNVLLNTFQFFGLNCS 270

RESULT 19
US-09-826-509-477
Sequence 477, Application US/09826509
Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin

;; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
;; FILE REFERENCE: Protein-Coupled Receptors
;; CURRENT APPLICATION NUMBER: US/09/826,509
;; CURRENT FILING DATE: 2001-04-05
;; PRIOR APPLICATION NUMBER: 60/195,747
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: 09/170,496
;; PRIOR FILING DATE: 1998-10-13
;; NUMBER OF SEQ ID NOS: 589
;; SOFTWARE: PatentIn Version 2.1
;; SEQ ID NO 477
;; LENGTH: 352
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-826-509-477

Query Match 100.0%; Score 118; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 20
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Schweickart, Vicky L.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-2

Query Match 100.0%; Score 118; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 22
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCRS) HDGPR10
; FILE REFERENCE: 1488.115000N
US-10-106-623-2

Query Match 100.0%; Score 118; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 21
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Schweickart, Vicky L.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20

Query Match 100.0%; Score 118; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
DB 249 APYNIVLLNTFQFFGLNCS 270

RESULT 22
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCRS) HDGPR10
; FILE REFERENCE: 1488.115000N
US-10-106-623-2

; CURRENT APPLICATION NUMBER: US/10/232,686
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
DB 249 APYNVLLNTFQFFGLNCS 270

RESULT 23

US-10-086-814-1
; Sequence 1, Application US/1006814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana C.
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
DB 249 APYNVLLNTFQFFGLNCS 270

RESULT 24

US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
DB 249 APYNVLLNTFQFFGLNCS 270

RESULT 25

US-10-067-800-22
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-22

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
DB 249 APYNVLLNTFQFFGLNCS 270

RESULT 26

US-10-290-058A-6
; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524
; FILE REFERENCE: MP101-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07


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; PRIOR APPLICATION NUMBER: 60/344,352
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match      100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APYNIVLLNTFOEFFGLNCS 22
        |||||
Db      249 APYNIVLLNTFOEFFGLNCS 270

RESULT 27
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match      100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APYNIVLLNTFOEFFGLNCS 22
        |||||
Db      249 APYNIVLLNTFOEFFGLNCS 270

RESULT 28
US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/MAP/DUK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-10-323-314-1

Query Match      100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 APYNIVLLNTFOEFFGLNCS 22
        |||||
Db      249 APYNIVLLNTFOEFFGLNCS 270

RESULT 29
US-10-072-301-1
; Sequence 1, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-1

Query Match      100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APYNIVLLNTFOEFFGLNCS 22
        |||||
Db      249 APYNIVLLNTFOEFFGLNCS 270

RESULT 30
US-10-164-649-52
; Sequence 52, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52

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Query Match      100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 APYNIIVLLINTFQEFFGLNCS 22
      |||||
Db      249 APYNIIVLLINTFQEFFGLNCS 270

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Search completed: March 4, 2004, 18:22:53
Job time : 30.4082 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 42.7959 Seconds
(without alignment)
118.840 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFNLYVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: A Geneseq 23Jan04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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4	95	100.0	43	5	AAE14756
5	95	100.0	58	5	AAE14759
6	95	100.0	58	5	AAE14755
7	95	100.0	268	7	ADC10142
8	95	100.0	268	7	ADC10144
9	95	100.0	332	2	AAW26766
10	95	100.0	352	2	AAW27407
11	95	100.0	352	2	AAW27123
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13	95	100.0	352	2	AAW07602
14	95	100.0	352	2	AAW23835
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16	95	100.0	352	3	AAE180128
17	95	100.0	352	4	AAE079089
18	95	100.0	352	4	AAE07046
19	95	100.0	352	4	AAE07048
20	95	100.0	352	4	AAE080111
21	95	100.0	352	4	AAE04321
22	95	100.0	352	4	AAE07037
23	95	100.0	352	4	AAE07039
24	95	100.0	352	4	AAE46858
25	95	100.0	352	4	ABE56342
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51	80	84.2	354	2	AAW54037
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54	79	83.2	360	4	AAW80108
55	79	83.2	360	4	AAU07613
56	79	83.2	360	4	AAU07614
57	79	83.2	360	4	ABE56340
58	79	83.2	360	6	ABP97725
59	79	83.2	360	6	ABP81987
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87	65	68.4	332	5	ABJ03698
88	65	68.4	332	5	ABJ03698
89	65	68.4	332	5	ABJ03698
90	65	68.4	332	5	ABJ03698
91	65	68.4	332	5	ABJ03698
92	65	68.4	332	5	ABJ03698
93	65	68.4	332	5	ABJ03698
94	65	68.4	332	5	ABJ03698
95	65	68.4	332	5	ABJ03698
96	65	68.4	332	5	ABJ03698
97	65	68.4	332	5	ABJ03698
98	65	68.4	332	5	ABJ03698

AAB83354 Human CCR
AAB82948 Human HIV
AAU97150 Human G-p
AAU97152 Human G-p
AAM52829 Human CCR
AAM52828 Human CC
ABG70597 Human G-p
ABG92883 Human imm
ABG92880 Human G-p
AAE25808 Human G-p
AAE25811 Human G-p
AAB81034 G-protein
ABE08343 Human che
ABG75540 Human G-p
ABE56602 Human can
AAO29514 Human C-C
ABU61654 Human G-p
ABP97728 Amino aci
ABP81933 Human C-C
ADC03341 Human che
ADC03359 Macaque c
AAW23834 Human CC
AAW41280 Fusion pr
ADD44859 Rat Prote
ADD44863 Rat Prote
AAW54037 Mouse CC-
AAW79166 Human mon
AAW35833 Human mon
AAW80108 Human CCR
AAU07613 Human CCR
AAU07614 Human wil
ABE56340 Non-endog
ABP97725 Amino aci
ABP81987 Human C-C
ABE88983 HIV gp120
ABE88981 HIV gp120
AAE14758 Human CCR
AAW03377 CC-chemok
AAW03376 CC-chemok
AAW03377 CC-chemok
AAW10100 Human C-C
AAW27124 Human che
AAW1850 Human eos
AAW51744 Human C-C
AAW51745 Human C-C
AAW80109 Human CCR
ABE56341 Non-endog
AAE15320 Human che
ABE07240 Human CC
ABE79520 Monkey C-
ABE07733 Human C-C
ABG72634 Human C-C
ABU09084 Human che
ABP97726 Amino aci
ABP81791 Human C-C
ADC03343 Human che
AAW25943 Human CCR
AAW78873 Human PRO
AAW07618 Human G-p
AAW49807 Human G-p
AAW56689 Human MCP
AAW97868 Human CC
AAW80115 Human CCR
ABE56343 Non-endog
AAU80222 Human che
AAU77932 Human G-p
ABP97731 Amino aci
ABP81794 Human C-C
AAU77933 Human G-p
ABP81684 G protein
AAW29179 Rat CC ch
ADD45360 Rat Prote
AAW48086 Human den

99 61 64.2 365 3 AAY97077 Primate (

100 61 64.2 365 6 ABU09080 Human den

ALIGNMENTS

RESULT 1
AAB88982
ID AAB88982 standard; peptide; 18 AA.
XX
AC AAB88982;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #75.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PS (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
DR WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.
XX
PS Claim 21; Page 38; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 1 YAFVGEKFRNLLVFFQK 18

RESULT 2
AAB88997
ID AAB88997 standard; peptide; 18 AA.
XX
AC AAB88997;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #90.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.

Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 1 YAFVGEKFRNLLVFFQK 18

RESULT 3
AAE14757
ID AAE14757 standard; peptide; 27 AA.
XX
AC AAE14757;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human CCR5 chemokine receptor deletion mutant fragment (aa 295-321).
XX
KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;
KW human immunodeficiency virus; gene therapy; human; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.

Query Match 100.0%; Score 95; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 1 YAFVGEKFRNLLVFFQK 18

Key Location/Qualifiers
FT Misc-difference 27 /note= "wild-type Cys replaced by Glx"

EP1207202-A1.

22-MAY-2002.

12-NOV-2001; 2001EP-00126500.

16-NOV-2000; 2000EP-00125052.

(MOEL/) MOELLING K.

Moelling K, Schwenker M;

WPI; 2002-437464/47.

Nucleic acid encoding a protein which interacts with the carboxy terminus

PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library
 PT is useful to detect, treat and prevent HIV infection.
 XX Example 2; Fig 2A; 28pp; English.

CC The invention relates to nucleic acid encoding a protein which interacts
 CC with the carboxy terminus of the chemokine receptor CCR5 or of other
 CC chemokine receptor family members. Molecules of the invention are used to
 CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
 CC -derived peptides, or compounds derived from the protein of the invention
 CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
 CC of the invention would block HIV infection. The present sequence is human
 CC chemokine receptor CCR5 C-terminal fragment deletion mutant which is
 CC incapable of interacting with the protein of the invention
 XX

XX Sequence 27 AA;

Query Match 100.0%; Score 95; DB 5; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 Db 3 YAFVGEKFRNYLLVFFQK 20

RESULT 4

AAE14756
 ID AAE14756 standard; peptide; 43 AA.

XX AAE14756;

DT 04-OCT-2002 (first entry)

DE Human CCR5 chemokine receptor deletion mutant fragment (aa 295-337).

KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;

KW human immunodeficiency virus; gene therapy; human; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 43 /note= "Wild-type Ser replaced by Glx"

XX EPI207202-A1.

XX 22-MAY-2002.

XX 12-NOV-2001; 2001EP-00126500.

XX 16-NOV-2000; 2000EP-00125052.

XX (MOEL/) MOELLING K.

XX Moelling K, Schwenecker M;

XX WPI; 2002-437464/47.

XX Nucleic acid encoding a protein which interacts with the carboxy terminus
 PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library
 PT is useful to detect, treat and prevent HIV infection.

XX Example 2; Fig 2A; 28pp; English.

CC The invention relates to nucleic acid encoding a protein which interacts
 CC with the carboxy terminus of the chemokine receptor CCR5 or of other
 CC chemokine receptor family members. Molecules of the invention are used to
 CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
 CC -derived peptides, or compounds derived from the protein of the invention
 CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
 CC of the invention would block HIV infection. The present sequence is human

CC chemokine receptor CCR5 C-terminal fragment deletion mutant which is
 CC incapable of interacting with the protein of the invention
 XX

XX Sequence 43 AA;

Query Match 100.0%; Score 95; DB 5; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 Db 3 YAFVGEKFRNYLLVFFQK 20

RESULT 5

AAE14759
 ID AAE14759 standard; peptide; 58 AA.

XX AAE14759;

DT 04-OCT-2002 (first entry)

DE Human CCR5 chemokine receptor C-terminal mutant fragment (aa 295-352).

KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;

KW human immunodeficiency virus; gene therapy; human; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 58 /note= "Wild-type Leu replaced by Pro"

XX EPI207202-A1.

XX 22-MAY-2002.

XX 12-NOV-2001; 2001EP-00126500.

XX 16-NOV-2000; 2000EP-00125052.

XX (MOEL/) MOELLING K.

XX Moelling K, Schwenecker M;

XX WPI; 2002-437464/47.

XX Nucleic acid encoding a protein which interacts with the carboxy terminus
 PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library
 PT is useful to detect, treat and prevent HIV infection.

XX Example 2; Fig 2A; 28pp; English.

CC The invention relates to nucleic acid encoding a protein which interacts
 CC with the carboxy terminus of the chemokine receptor CCR5 or of other
 CC chemokine receptor family members. Molecules of the invention are used to
 CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
 CC -derived peptides, or compounds derived from the protein of the invention
 CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
 CC of the invention would block HIV infection. The present sequence is human
 CC chemokine receptor CCR5 C-terminal mutant fragment which is incapable of
 CC interacting with the protein of the invention
 XX

XX Sequence 58 AA;

Query Match 100.0%; Score 95; DB 5; Length 58;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 Db 3 YAFVGEKFRNYLLVFFQK 20

RESULT 6
AAE14755
ID AAE14755 standard; peptide; 58 AA.
XX AC AAE14755;
XX DT 04-OCT-2002 (first entry)
XX DE Human CCR5 chemokine receptor C-terminal fragment (residues 295-352).
XX KW Chemokine receptor CCR5; p2 protein; HIV infection;
XX KW human immunodeficiency virus; AIDS; gene therapy; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Binding-eite 58
FT /note= "Essential for binding to human protein P2
FT (AAE14754)"
XX EP1207202-A1.
XX PN 22-MAY-2002.
XX PD 12-NOV-2001; 2001EP-00126500.
XX PF 16-NOV-2000; 2000EP-00125052.
XX PR (MOEL/) MOELLING K.
XX PA Moelling K, Schwenecker M;
XX PI WPI; 2002-437464/47.
XX DR Nucleic acid encoding a protein which interacts with the carboxy terminus
XX PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library
XX PT is useful to detect, treat and prevent HIV infection.
XX PS Example 2; Fig 2A; 28pp; English.
XX CC The invention relates to nucleic acid encoding a protein which interacts
XX CC with the carboxy terminus of the chemokine receptor CCR5 or of other
XX CC chemokine receptor family members. Molecules of the invention are used to
XX CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5
XX CC -derived peptides, or compounds derived from the protein of the invention
XX CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein
XX CC of the invention would block HIV infection. The present sequence is human
XX CC chemokine receptor CCR5 C-terminal fragment
XX SQ Sequence 58 AA;
Query Match 100.0%; Score 95; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | | | | | |
Db 3 YAFVGEKFRNLLVFFQK 20
RESULT 7
ADCI0142
ID ADCI0142 standard; protein; 268 AA.
XX AC ADCI0142;
XX DT 18-DEC-2003 (first entry)
XX DE Human NOVX polypeptide SEQ ID NO: 162.
XX KW cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;

KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
KW inflammatory disorder; chromosome mapping; tissue typing;
XX OS Homo sapiens.
XX PN WO2003000842-A2.
XX PD 03-JAN-2003.
XX PF 04-JUN-2002; 2002WO-US017443.
XX PR 04-JUN-2001; 2001US-0295607P.
XX PR 04-JUN-2001; 2001US-0295661P.
XX PR 06-JUN-2001; 2001US-0296404P.
XX PR 06-JUN-2001; 2001US-0296418P.
XX PR 07-JUN-2001; 2001US-0296575P.
XX PR 11-JUN-2001; 2001US-0297414P.
XX PR 12-JUN-2001; 2001US-0295573P.
XX PR 12-JUN-2001; 2001US-0297567P.
XX PR 14-JUN-2001; 2001US-0298285P.
XX PR 15-JUN-2001; 2001US-0298528P.
XX PR 18-JUN-2001; 2001US-0299133P.
XX PR 19-JUN-2001; 2001US-0299230P.
XX PR 21-JUN-2001; 2001US-0299949P.
XX PR 22-JUN-2001; 2001US-0300177P.
XX PR 26-JUN-2001; 2001US-0300883P.
XX PR 28-JUN-2001; 2001US-0301530P.
XX PR 28-JUN-2001; 2001US-0301550P.
XX PR 03-JUL-2001; 2001US-0302951P.
XX PR 31-JUL-2001; 2001US-0308890P.
XX PR 14-SEP-2001; 2001US-0322297P.
XX PR 25-SEP-2001; 2001US-0324659P.
XX PR 03-DEC-2001; 2001US-0337477P.
XX PR 14-DEC-2001; 2001US-0341562P.
XX PR 21-FEB-2002; 2002US-0358656P.
XX PR 21-FEB-2002; 2002US-0359132P.
XX PR 22-FEB-2002; 2002US-0358978P.
XX PR 22-FEB-2002; 2002US-0359034P.
XX PR 22-FEB-2002; 2002US-0359035P.
XX PR 22-FEB-2002; 2002US-0359121P.
XX PR 27-FEB-2002; 2002US-0359964P.
XX PR 01-MAR-2002; 2002US-0360858P.
XX PR 12-MAR-2002; 2002US-0363430P.
XX PR 12-MAR-2002; 2002US-0363676P.
XX PR 10-APR-2002; 2002US-0371346P.
XX PR 10-MAY-2002; 2002US-0379444P.
XX PR 04-JUN-2002; 2002US-00379444.
XX PA (CURA-) CURAGEN CORP.
XX FI Agee ML, Anderson DW, Berghs C, Caaman SJ, Catterton E;
FI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
FI Geflach VI, Gorman L, Guo X, Herrmann JL, Hjalte T, Ji W, Kekuda R;
FI Khrantsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
FI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
FI Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna SK;
FI Spytke KA, Stone DJ, Vernet CM, Zhong H, Zhong M, Alsobrook JP;
FI Burgess CE, Lepley DM;
XX WPI; 2003-210149/20.
XX N-PSDB; ADCI0141.
XX PT New isolated NOVX polypeptides and nucleic acid molecules useful for
XX PT treating, preventing and diagnosing pathological conditions with NOVX-
XX PT associated disorders, such as cancer, obesity, diabetes and inflammatory
XX PT or CNS diseases.
XX PS Claim 1; SEQ ID NO 162; 772pp; English.
XX CC The invention relates to novel isolated polypeptides, mature form of the
XX CC polypeptide, a sequence that is 95% identical to the polypeptide or the

CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.

XX SQ Sequence 268 AA;

Query Match 100.0%; Score 95; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 DB 213 YAFVGEKFRNLLVFFQK 230

RESULT 8
 ADC10144
 ID ADC10144 standard; protein; 268 AA.

XX AC ADC10144;
 XX DT 18-DEC-2003 (first entry)
 XX DE Human NOVX polypeptide SEQ ID NO: 164.

XX cytotatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
 KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
 KW inflammatory disorder; chromosome mapping; tissue typing;
 KW predictive medicine.

XX OS Homo sapiens.

XX PN WC2003000842-A2.

XX PD 03-JAN-2003.

XX PF 04-JUN-2002; 2002WO-US017443.

XX PR 04-JUN-2001; 2001US-0295607P.

XX PR 04-JUN-2001; 2001US-0295661P.

XX PR 06-JUN-2001; 2001US-0296404P.

XX PR 06-JUN-2001; 2001US-0296418P.

XX PR 07-JUN-2001; 2001US-0296575P.

XX PR 11-JUN-2001; 2001US-0297414P.

XX PR 12-JUN-2001; 2001US-0295573P.

XX PR 12-JUN-2001; 2001US-0297567P.

XX PR 14-JUN-2001; 2001US-0298285P.

XX PR 15-JUN-2001; 2001US-0298528P.

XX PR 18-JUN-2001; 2001US-0299133P.

XX PR 19-JUN-2001; 2001US-0299230P.

XX PR 21-JUN-2001; 2001US-0299949P.

XX PR 22-JUN-2001; 2001US-0300177P.

XX PR 26-JUN-2001; 2001US-0300883P.

XX PR 28-JUN-2001; 2001US-0301530P.

XX PR 28-JUN-2001; 2001US-0301550P.

XX PR 03-JUL-2001; 2001US-0302951P.

PR 27-FEB-2002; 2002US-0359364P.
 PR 01-MAR-2002; 2002US-0360858P.
 PR 12-MAR-2002; 2002US-0363430P.
 PR 12-MAR-2002; 2002US-0363676P.
 PR 10-APR-2002; 2002US-0371346P.
 PR 10-MAY-2002; 2002US-0379444P.
 PR 04-JUN-2002; 2002US-00379444.

XX (CURA-) CURAGEN CORP.

XX AGee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;
 PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
 PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;
 PI Khramsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;
 PI Ort T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;
 PI Rdthenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;
 PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;
 PI Burges CE, Lepley DM;

XX WPI; 2003-210149/20.
 DR N-PSDB; ADC10143.

XX New isolated NOVX polypeptides and nucleic acid molecules useful for
 PT treating, preventing and diagnosing pathological conditions with NOVX-
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory
 PT or CNS diseases.

XX Claim 1; SEQ ID NO 164; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to one of the
 CC polypeptides of the invention.

XX SQ Sequence 268 AA;

Query Match 100.0%; Score 95; DB 7; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 213 YAFVGEKFRNLLVFFQK 230

RESULT 9

AAW26766
 ID AAW26766 standard; protein; 332 AA.

XX AAW26766;

XX 21-MAY-1998 (first entry)

XX Human chemokine receptor MMLR-CCR.

XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;
 KW monocyte; macrophage; chemotaxis; haematopoiesis; infection;
 KW inflammation; proliferative disease; cardiovascular disease; tumour;
 KW rheumatoid arthritis; alveolitis; atherosclerosis;
 KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;
 KW inflammatory bowel disease; toxic shock syndrome; septic shock;
 KW Chediak-Higashi syndrome; therapy; diagnosis.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 107..128

FT Misc-difference 121 /note= "conserved peptide"
 FT 121
 FT /note= "a claimed polypeptide has isoleucine at residue
 FT 121"
 XX
 PN WO9741225-A2.
 XX
 PD 06-NOV-1997.
 XX
 PF 25-APR-1997; 97WO-US006993.
 XX
 PR 26-APR-1996; 96US-00638081.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Au-Young J, Bandman O, Coleman R, Wilde CG;
 XX
 DR WPI; 1997-549729/50.
 XX
 DR N-PSDB; AAT99542.
 XX
 XX Polynucleotide encoding MMLR-CCR or MPH-CCR chemokine receptor - useful
 PT to study, diagnose and treat, e.g. infection, inflammation, solid tumour
 PT and proliferative and cardiovascular disease.
 XX
 PS Claim 8; Page 37-38; 59pp; English.
 XX
 CC This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
 CC associated with monocyte/macrophage infiltration and chemotaxis and
 CC haematopoiesis. The amino acid sequence was deduced from a cDNA clone
 CC (see AAT99542) obtained from a cDNA library made from mononuclear cells
 CC collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
 CC with inflammation and immunomodulation. Another novel chemokine receptor,
 CC MPH-CCR (see AAT36767), is also claimed. MMLR-CCR contains 7
 CC transmembrane spanning segments connected by a series of intracellular
 CC and extracellular loops. MMLR-CCR and MPH-CCR can be used to study,
 CC diagnose and treat disease states in which normal leukocyte function is
 CC perturbed by normal leukopoiesis or inappropriate activation via
 CC chemokine agonists or antagonists, such as infection, inflammation,
 CC proliferative disease, tumorigenesis, autoimmune disease, abnormal cell
 CC proliferation, solid tumours, cardiovascular disease, rheumatoid
 CC arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
 CC asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
 CC shock syndrome, septic shock and Chediak-Higashi syndrome
 XX
 SQ Sequence 332 AA;
 Query Match 100.0%; Score 95; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFNRYLLVFFQK 18
 |||||
 Db 277 YAFVGEKFNRYLLVFFQK 294
 |||||
 RESULT 10
 AAW27407
 ID AAW27407 standard; protein; 352 AA.
 XX
 AC AAW27407;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Human CCR5.
 XX
 KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX
 OS Homo sapiens.
 XX

PN WO9732019-A2.
 XX
 PD 04-SEP-1997.
 XX
 PF 28-FEB-1997; 97WO-BE000023.
 XX
 PR 01-MAR-1996; 96EP-00870021.
 XX
 PR 06-AUG-1996; 96EP-00870102.
 XX
 PA (EURO-) EUROSREEN SA.
 XX
 PI Samson M, Parmentier M, Vassart G, Libert F;
 XX
 DR WPI; 1997-479829/44.
 XX
 DR N-PSDB; AAT90117.
 XX
 XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX
 PS Claim 4; Fig 1b-c; 94pp; English.
 XX
 CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
 CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, but
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 95; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFNRYLLVFFQK 18
 |||||
 Db 297 YAFVGEKFNRYLLVFFQK 314
 |||||
 RESULT 11
 AAW27123
 ID AAW27123 standard; protein; 352 AA.
 XX
 AC AAW27123;
 XX
 DT 14-DEC-1997 (first entry)
 XX
 DE Human chemokine receptor 88C.
 XX
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 KW modulator; antibody; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..32 /label= Extracellular_domain
 FT Domain 56..67 /label= Intracellular_domain
 FT Domain 89..112 /label= Extracellular_domain
 FT Domain 125..145 /label= Extracellular_domain
 FT Domain 166..191 /label= Intracellular_domain
 FT Domain 213..235 /label= Extracellular_domain


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FT Domain /label= Intracellular_domain
FT 259..280
FT /label= Extracellular_domain
FT 301..352
FT /label= Intracellular_domain
XX WO9722698-A2.
XX
XX PD 26-JUN-1997.
XX
XX PF 20-DEC-1996; 96WO-US020759.
XX PR 20-DEC-1995; 95US-00575967.
XX PR 07-JUN-1996; 96US-00661393.
XX PA (ICOS-) ICOS CORP.
XX
XX PI Gray PW, Schweickart VL, Raport CJ;
XX WPI; 1997-341689/31.
XX DR N-PSDB; AAT85161.
XX
XX PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX PT tumours, viral infections, auto-immune diseases, etc.
XX
XX PS Claim 16; Page 47-48; 65pp; English.
XX
XX CC This polypeptide sequence comprises novel human chemokine receptor 88C, a
XX CC G protein coupled receptor that is involved in leukocyte trafficking. Its
XX CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
XX CC macrophage library. It shows 62% identity to CCKR1. Chemokine receptor
XX CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
XX CC and their polypeptide fragments can be produced in transformed host
XX CC cells. The receptors, peptides comprising one or more of the
XX CC extracellular or intracellular domains, and anti-receptor antibodies can
XX CC be used to modulate receptor activities, particularly ligand and G
XX CC protein binding, and are potentially useful in the treatment
XX CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX CC infection, AIDS, inflammatory conditions, pathological immune response,
XX CC abnormal haematopoietic processes etc
XX SQ Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNLLVFFQK 18
XX |||||
XX Db 297 YAFVGEKFRNLLVFFQK 314
XX
XX RESULT 12
XX AAW27125
XX ID AAW27125 standard; protein; 352 AA.
XX AC AAW27125;
XX
XX DT 14-DEC-1997 (first entry)
XX
XX DE Macaque chemokine receptor 88C.
XX
XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX KW modulator; antibody.
XX
XX OS Macaca sp.
XX
XX PN WO9722698-A2.
XX
XX PD 26-JUN-1997.

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XX PF 20-DEC-1996; 96WO-US020759.
XX PR 20-DEC-1995; 95US-00575967.
XX PR 07-JUN-1996; 96US-00661393.
XX PA (ICOS-) ICOS CORP.
XX
XX PI Gray PW, Schweickart VL, Raport CJ;
XX WPI; 1997-341689/31.
XX DR N-PSDB; AAT85163.
XX
XX PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX PT tumours, viral infections, auto-immune diseases, etc.
XX
XX PS Claim 36; Page 57-58; 65pp; English.
XX
XX CC This polypeptide sequence comprises macaque chemokine receptor 88C, a G
XX CC protein coupled receptor that is involved in leukocyte trafficking. Its
XX CC amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX CC amplification. It shows 9% identity to human 88C (AAW27123). 88C
XX CC receptors and their polypeptide fragments can be produced in transformed
XX CC host cells. The receptors, peptides comprising one or more of the
XX CC extracellular or intracellular domains, and anti-receptor antibodies can
XX CC be used to modulate receptor activities, particularly ligand and G
XX CC protein binding, and are potentially useful in the treatment
XX CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX CC infection, AIDS, inflammatory conditions, pathological immune response,
XX CC abnormal haematopoietic processes etc. A hybridoma that produces an
XX CC antibody that specifically binds to macaque 88C is claimed
XX SQ Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNLLVFFQK 18
XX |||||
XX Db 297 YAFVGEKFRNLLVFFQK 314
XX
XX RESULT 13
XX AAW07602
XX ID AAW07602 standard; protein; 352 AA.
XX AC AAW07602;
XX
XX DT 26-FEB-1997 (first entry)
XX
XX DE Human G-protein chemokine receptor HDGMR10.
XX
XX KW G-protein chemokine receptor; HDGMR10; signal transduction;
XX KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
XX KW therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO9639437-A1.
XX
XX PD 12-DEC-1996.
XX
XX PF 06-JUN-1995; 95WO-US007173.
XX PR 06-JUN-1995; 95WO-US007173.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Li Y, Ruben SM;
XX
XX PD WPI; 1997-043072/04.

```

DR N-PSDB; AAT44042.
 XX Human G-protein chemokine receptor, HDGNR10 - useful to identify
 FT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
 FT acute inflammation, rheumatoid arthritis, etc.
 XX
 XX Claim 1; Page 44-46; 61pp; English.
 XX
 CC Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7
 CC -transmembrane protein involved in signal transduction. Its amino acid
 CC sequence was deduced from a cDNA clone (AAI44042) isolated from a human
 CC monocyte library. Isolation of the cDNA allows prodn. of recombinant
 CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
 CC receptor can be used to identify agonists or antagonists of the receptor;
 CC such cpds. can be used to treat conditions related to the under- and over
 CC -expression of G-protein chemokine receptors
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 95; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 297 YAFVGEKFRNLLVFFQK 314
 RESULT 14
 AAW23835
 ID AAW23835 standard; protein; 352 AA.
 AC AAW23835;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Human CC chemokine receptor 5 (CCR5).
 XX
 CC Chemokine receptor 5; CCR5; G-protein coupled receptor;
 XX human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 29..55
 FT /label= I
 FT /note= "transmembrane domain"
 FT 104..126
 FT /label= III
 FT /note= "transmembrane domain"
 FT 109..120
 FT /note= "extracellular loop-1 (Claim 19)"
 FT 143..171
 FT /label= IV
 FT /note= "transmembrane domain"
 FT 187..210
 FT /note= "extracellular loop-2 (Claim 19)"
 FT 194..219
 FT /label= V
 FT /note= "transmembrane domain"
 FT 238..258
 FT /label= VI
 FT /note= "transmembrane domain"
 FT 261..276
 FT /note= "extracellular loop-3 (Claim 19)"
 FT 277..300
 FT /label= VII
 FT /note= "transmembrane domain"
 XX WC9745543-A2.
 XX
 PD 04-DEC-1997.
 XX

PF 28-MAY-1997; 97WO-US009586.
 XX
 PR 28-MAY-1996; 96US-0018508P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Combadriere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
 PI Broder CC, Kennedy PE;
 XX
 WPI: 1998-032650/03.
 DR N-PSDB; AAT76920.
 XX
 CC Chemokine receptor 5 polypeptide - used to inhibit membrane fusion
 FT between HIV and a target cell.
 XX
 XX Claim 68; Fig 1C; 70pp; English.
 XX
 CC This protein sequence comprises of a novel human macrophage-selective CC
 CC chemokine receptor that has been designated CCR5. The sequence was
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant
 CC (see W238340 of CCR5 was also identified. The susceptibility of human
 CC macrophages to HIV infection depends on cell surface expression of CD4
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
 CC protein coupled cell surface molecules. It plays an essential role in the
 CC membrane fusion step of infection by some HIV isolates. The establishment
 CC of stable, non-human cell lines and transgenic mammals having cells that
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
 CC agents capable of blocking membrane fusion between HIV and target cells
 CC represent potential anti-HIV therapeutics for macrophage tropic strains
 CC of HIV
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 95; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 297 YAFVGEKFRNLLVFFQK 314
 RESULT 15
 AAW88232
 ID AAW88232 standard; protein; 352 AA.
 XX
 AC AAW88232;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE HIV-1 co-receptor CCR5.
 XX
 KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
 XX gene therapy; human.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 32..56
 FT /note= "transmembrane domain 1"
 FT 67..87
 FT /note= "transmembrane domain 2"
 FT /note= "Misc-difference 101"
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA
 FT (Stop) in CCR5m303"
 FT 103..124
 FT /note= "transmembrane domain 3"
 FT 142..167
 FT /note= "transmembrane domain 4"
 FT 200..223
 FT /note= "transmembrane domain 5"
 FT 236..260
 FT Domain

FT /note= "transmembrane domain 6"
 FT 275...301
 FT /note= "transmembrane domain 7"

XX W09854317-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-EP003437.

XX 30-MAY-1997; 97US-0048057P.

XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;

XX WPI; 1999-059835/05.

XX N-PSDB; AA84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
 PT resistance of CCR5-expressing cells to HIV-1 infection.

XX Disclosure; Page 34-35; 55pp; English.

CC This is the amino acid sequence of wild-type human CCR5, which serves as
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see
 CC AA88231), designated CCR5m303, comprising the first two transmembrane
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a
 CC positive correlation with resistance to infection with M-tropic HIV-1
 CC strains, and may indicate slower progression of the disease. The
 CC detection of CCR5 variants may be used to identify individuals at lower
 CC risk of infection relative to the general population who, if infected,
 CC may exhibit slower progression to AIDS. Probes and primers (see AA84127-
 CC 36) are provided for use in diagnostic methods for detecting the presence
 CC of such variants. A method is provided for inhibiting HIV-1 infection of
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number
 CC of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNVLVFFQK 314

RESULT 16

AA80128
 ID AA80128 standard; protein; 352 AA.

XX AC AA80128;

XX 19-MAY-2000 (first entry)

XX Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.

XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;
 KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
 KW tumour; infection; leukaemia; psoriasis; allergy;
 KW T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
 KW inflammation; allergic reaction; silicosis; sarcoidosis;
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.

XX Homo sapiens.

XX US6025154-A.

XX

PD 15-FEB-2000.

XX 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI; 2000-181807/16.

XX N-PSDB; AA291481.

XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
 PT for diagnostic assays, scientific research and screening for compounds
 PT which bind to and activate or inhibit activation of the receptor
 PT polypeptides.

XX Claim 1; Fig 1; 22pp; English.

XX The present sequence represents a human G-protein chemokine receptor
 CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of
 CC screening for compounds which bind to and either: (1) activate the
 CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound
 CC healing, coagulation, and angiogenesis; treatment of solid tumours,
 CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,
 CC parasitic infections, psoriasis, and to stimulate growth factor activity;
 CC or (2) inhibit activation of the HDGNR10 polypeptides which is useful for
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for
 CC diagnostic assays for detecting diseases related to mutations in the
 CC nucleic acid sequences encoding the polypeptides and for detecting an
 CC altered level of the soluble form of the receptor polypeptides. The
 CC polynucleotides are also useful for in vitro purposes related to
 CC scientific research, synthesis of DNA and manufacture of DNA vectors
 XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNVLVFFQK 314

RESULT 17

AA879089
 ID AA879089 standard; protein; 352 AA.

XX AC AA879089;

XX 10-DEC-2001 (first entry)

XX Amino acid sequence of human CCR5 protein.

XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.

XX Homo sapiens.

XX WO200164752-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006322.

XX 02-MAR-2000; 2000US-00517605.

XX

CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 19

AAE07048
 ID AAE07048 standard; protein; 352 AA.

XX AC AAE07048;

XX DT 16-OCT-2001 (first entry)

XX DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.

XX KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX OS Homo sapiens.

XX PN WO200158916-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004153.

XX PR 09-FEB-2000; 2000US-0181258P.

XX PR 09-MAR-2000; 2000US-0187999P.

XX PR 22-SEP-2000; 2000US-0234336P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Roschke V, Li Y, Ruben SM;

XX DR WPI; 2001-488966/53.

XX DR N-PSDB; AAD13299.

XX PT Isolated nucleic acid encoding a human G-protein chemokine receptor

XX PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune

XX PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and

XX PT neurodegenerative disorders.

XX PS Example 40; Page 504-505; 518pp; English.

XX CC The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC disease or disorder may be associated with aberrant CCR5 expression, lack
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative

CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18

|||||
 DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 20

AAE01111
 ID AAG80111 standard; protein; 352 AA.

XX AC AAG80111;

XX DT 17-JAN-2002 (first entry)

XX DE Human CCR5 protein.

XX KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.

XX OS Homo sapiens.

XX PN WO200172830-A2.

XX PD 04-OCT-2001.

XX PF 02-APR-2001; 2001WO-EP003708.

XX PR 31-MAR-2000; 2000DE-01016013.

XX PA (IPFP-) IPF PHARM GMBH.

XX PA (FORS/) FORSMANN U.

XX PI Forssmann W, Adermann K, Heitland A, Spodsberg N;

XX DR WPI; 2001-626256/72.

XX PT Diagnostic agent containing two or more receptor-specific ligands, useful
 XX PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 XX PT inhibitors.

XX PS Disclosure; Page 10; 26pp; German.

XX CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.

CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 21
 AAE04321
 ID AAE04321 standard; protein; 352 AA.

AC AAE04321;
 DT 04-SEP-2001 (first entry)

DE Human chemokine receptor (CCR), CC-CR-5 related protein #2.

XX Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CR-5; envelope glycoprotein; anti-HIV.

XX Homo sapiens.

XX US5258527-B1.

XX 10-JUL-2001.

XX 21-MAY-1997; 97US-00861105.

XX 20-MAY-1996; 96US-0017157P.

PR 19-JUN-1996; 96US-0020043P.

PR 19-MAY-1997; 97US-00858660.

XX (AARO-) AARON DIAMOND AIDS RES CENT.

PA (UINY) UNIV NEW YORK STATE.

PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

DR N-PSDB; AAD08577.

XX Transformed mammalian cell (T) that contains a CD4 gene, reporter gene
 and HIV LTR for identification of drugs and antibodies for treatment of
 HIV.

XX Disclosure; Col 47-50; 37pp; English.

XX The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.
 CC CC-CR-5 is the principal cofactor for entry mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1

XX Sequence 352 AA;

SQ

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 22
 AAE07037
 ID AAE07037 standard; protein; 352 AA.

AC AAE07037;

DT 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 KW cytostatic; immunosuppressive; neutropenic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..36 /label= Extracellular_domain
 FT Domain 37..305 /label= Transmembrane_domain
 FT Domain 37..58 /label= Transmembrane_domain
 FT FT /note= "Segment 1"
 FT Domain 59..67 /label= Intracellular_loop_1
 FT Domain 68..88 /label= Transmembrane_domain
 FT FT /note= "Segment 2"
 FT Domain 89..102 /label= Extracellular_loop_1
 FT FT /label= Transmembrane_domain
 FT FT /note= "Segment 3"
 FT Domain 125..141 /label= Intracellular_loop_2
 FT FT /label= Transmembrane_domain
 FT FT /note= "Segment 4"
 FT Domain 167..195 /label= Extracellular_loop_2
 FT Domain 196..223 /label= Transmembrane_domain
 FT FT /note= "Segment 5"
 FT Domain 224..235 /label= Intracellular_loop_3
 FT FT /label= Transmembrane_domain
 FT FT /note= "Segment 6"
 FT Domain 261..274 /label= Extracellular_loop_3
 FT FT /label= Transmembrane_domain
 FT FT /note= "Segment 7"
 FT Domain 306..352 /label= Intracellular_domain
 XX

PN WO200158915-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US0004152.
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 DR N-PSDB; AAD13181.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX Claim 102; Fig 1; 495pp; English.
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a
 CC disease or disorder associated with inflammation, defective or aberrant
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 CC presenting cell interaction. The disease or disorder may also be an
 CC infectious disease (e.g. a viral infection such as an early stage HIV
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 CC disorder. The disease or disorder may be associated with aberrant CCR5
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food
 CC additive or preservative to increase or decrease storage capabilities.
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists
 CC are also useful in the diagnosis, treatment and prevention of cancer
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound
 CC healing
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 297 YAFVGEKFRNLLVFFQK 314
 RESULT 23
 AAE07039
 ID AAE07039 standard; protein; 352 AA.
 XX AAE07039;
 AC AAE07039;
 XX 16-OCT-2001 (first entry)
 DT Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;

KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX Homo sapiens.
 OS WO200158915-A2.
 PN 16-AUG-2001.
 PD 09-FEB-2001; 2001WO-US0004152.
 XX 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Roschke V, Li Y, Ruben SM;
 PI WPI; 2001-488965/53.
 DR N-PSDB; AAD13198.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.
 XX Example 40; Page 486-487; 495pp; English.
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10
 CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or
 CC ameliorating a disease or disorder associated with inflammation, such as
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 CC aberrant T-cell antigen presenting cell interaction. The disease or
 CC disorder may also be an infectious disease (e.g. a viral infection such
 CC as an early stage HIV infection, a cytomegalovirus infection, or a
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 CC a neurodegenerative disorder. The disease or disorder may be associated
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein
 CC is used as a food additive or preservative to increase or decrease
 CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome
 CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,
 CC antibodies, agonists and antagonists are also useful in the diagnosis,
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular
 CC disorders (myocardial ischaemias) and wound healing
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 DB 297 YAFVGEKFRNLLVFFQK 314
 RESULT 24
 AAB46858
 ID AAB46858 standard; protein; 352 AA.
 XX AAB46858;
 AC AAB46858;
 DT 16-AUG-2001 (revised)

DT 02-AUG-2001 (revised)
 DT 04-MAY-2001 (first entry)
 DE Human HDGMR10 protein.
 XX
 XX HDGMR10; human; G-protein chemokine receptor; anti-inflammatory;
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
 KW cytotactic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
 KW hyper-eosinophilic syndrome; vulnery.
 XX
 XX Homo sapiens.
 XX
 XX US2001000241-A1.
 XX
 XX 12-APR-2001.
 XX
 XX 29-NOV-2000; 2000US-00725285.
 XX
 XX 06-JUN-1995; 95US-00466343.
 XX 18-NOV-1998; 98US-00195662.
 XX 25-JUN-1999; 99US-00339912.
 XX
 XX (LIYY/) LI Y.
 XX (RUBE/) RUBEN S. M.
 XX
 XX Li Y, Ruben SM;
 XX
 XX WPI; 2001-226317/23.
 XX N-PSDB; AAF26390.
 XX
 XX New human G-protein chemokine receptor polypeptides and polynucleotides,
 PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
 PT
 XX
 XX Claim 1a; Page 15; 2pp; English.
 XX
 XX This invention describes a novel receptor polypeptide (I) selected from
 CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
 CC products of the invention have antiinflammatory, immunomodulatory,
 CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,
 CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic
 CC activity and can be used for gene therapy. The G-protein chemokine
 CC receptors, HDGMR10, (I) are useful for screening for compounds which
 CC activate or inhibit activation of (I). The products of the invention can
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,
 CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
 CC stimulating growth factor activity. HDGMR10 is useful for treating
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
 CC reactions, prostaglandin-independent fever, bone marrow failure,
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
 CC errors in the keyword formatting)
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 25
 ABB56342
 ID ABB56342 standard; protein; 352 AA.
 XX
 XX AC ABB56342;
 XX
 XX 18-FEB-2002 (first entry)
 XX
 XX Non-endogenous human GPCR protein, SEQ ID NO: 477.
 DE
 XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
 KW constitutively activated GPCR; agonist; disease.
 KW
 XX Homo sapiens.
 XX OS Synthetic.
 XX
 XX WO200177172-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 05-APR-2001; 2001WO-US011098.
 XX
 XX 07-APR-2000; 2000US-0195747P.
 XX
 XX (AREN-) ARENA PHARM INC.
 XX
 XX Lehmann-Bruinsma K, Liaw CW, Lin I;
 XX
 XX WPI; 2001-648759/74.
 XX N-PSDB; ABI97978.
 XX
 XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in
 PT disease treatment, comprises contacting candidate compounds with versions
 PT of GPCRs.
 PT
 XX
 XX Claim 1; Page 277-278; 394pp; English.
 XX
 XX The invention relates to G protein-coupled receptors (GPCRs) for which
 CC the endogenous ligand has been identified. Non-endogenous constitutively
 CC activated versions of known GPCRs are used in the invention for the
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists. Such agonists are useful as
 CC therapeutic agents for diseases or disorders associated with GPCRs. The
 CC present sequence is a non-endogenous version of a known human GPCR.
 XX
 XX Sequence 352 AA;
 SQ

Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 26
 AAB83354
 ID AAB83354 standard; protein; 352 AA.
 XX
 XX AC AAB83354;
 XX
 XX 09-OCT-2001 (first entry)
 XX
 XX Human CCR5 protein sequence.
 DE
 XX Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;
 KW human immunodeficiency virus; anti-inflammatory disease; human.
 XX
 XX Homo sapiens.
 XX OS
 XX EP1118858-A2.
 XX

PD 25-JUL-2001.
 XX
 PF 03-JAN-2001; 2001EP-00300020.
 XX
 PR 12-JAN-2000; 2000GB-00000659.
 PR 12-JAN-2000; 2000GB-00000661.
 PR 12-JAN-2000; 2000GB-00000663.
 XX (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.
 XX
 XX Dobbs S, Perros M, Rickett GA;
 PI
 XX WPI; 2001-477088/52.
 DR N-PSDB; AAF87099.
 DR
 XX
 PT Determining if an agent can modulate CCR5-gp120 interaction, comprises
 PT incubating the agent with CCR5 and gp120 and determining if the agent
 PT modulates the interaction.
 XX
 PS Claim 1; Page 110; 113pp; English.
 XX
 CC This sequence represents the human CCR5 protein sequence. The invention
 CC relates to a method for determining whether an agent is capable of
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and
 CC determining whether the agent modulates the interaction, where gp120 is
 CC associated with CD4, and where the interaction is a low affinity binding.
 CC The method is used to identify an agent capable of modulating the
 CC interaction of CCR5 with gp120. An agent identified by the method is used
 CC to prepare a pharmaceutical composition for the treatment of a disease or
 CC condition associated with CCR5 and gp120 interaction, to treat a subject
 CC with a disease or condition associated with CCR5 and gp120 interaction,
 CC and for preparing a pharmaceutical for treating human immunodeficiency
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method
 CC is commercially useful, amenable to high throughput screening, and
 CC detects interaction of gp120 with cells expressing only CCR5
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNYLLVFFQK 18
 DB 297 YAFVGEKFRNYLLVFFQK 314
 RESULT 27
 AAB82948
 ID AAB82948 standard; protein; 352 AA.
 AC AAB82948;
 XX
 DT 21-DEC-2001 (first entry)
 XX
 DE Human HIV-1 co-receptor CCR5.
 XX
 XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;
 KW infection; therapy; vaccine; anti-HIV-1.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Binding-site 2..18
 FT /note= "binds to HIV-1 gp120"
 XX
 XX WO200164710-A2.
 PN
 XX
 XX 07-SEP-2001.
 PD
 XX
 XX 28-FEB-2001; 2001WO-US0006699.
 PF

XX 29-FEB-2000; 2000US-0185667P.
 PR 19-MAY-2000; 2000US-0205839P.
 PR 07-FEB-2001; 2001US-0267231P.
 XX
 PA (PROG-) PROGENICS PHARM INC.
 PA (AARO-) AARON DIAMOND AIDS RES CENT.
 XX
 XX Dragic T, Olson WC;
 XX
 XX WPI; 2001-611273/70.
 DR N-PSDB; AAH26903.
 XX
 PT Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-
 PT receptor) amino terminal domain including negatively charged and two
 PT sulfated tyrosine residues is useful for treating HIV infection in
 PT humans.
 XX
 XX Claim 1; Page 30; 163pp; English.
 XX
 CC The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids
 CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding
 CC site that determines the specificity of the interaction between CCR5 and
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the
 CC CCR5 N-terminus is required for gp120 binding and may critically modulate
 CC the susceptibility of target cells to HIV-1 infection in vivo. The
 CC invention provides claimed sulfated peptides (see AAB82947) that are
 CC based on the CCR5 N-terminal region and which are effective for
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+
 CC cells from becoming infected with HIV, of treating a subject whose CD4+
 CC cells are infected with HIV, and of identifying an agent which inhibits
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried
 CC out in a subject, especially a human, infected (therapeutic method), not
 CC infected with HIV (prophylactic method), or in a subject who is not
 CC infected with, but has been exposed to, HIV
 XX
 XX Sequence 352 AA;
 SQ
 Query Match 100.0%; Score 95; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNYLLVFFQK 18
 DB 297 YAFVGEKFRNYLLVFFQK 314
 RESULT 28
 AAU97150
 ID AAU97150 standard; protein; 352 AA.
 XX
 AC AAU97150;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.
 XX
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 XX Homo sapiens.
 OS
 XX US2002048786-A1.
 PN
 XX 25-APR-2002.
 PD
 XX 09-FEB-2001; 2001US-00779879.
 PF
 XX 09-FEB-2000; 2000US-0181258P.
 PR
 PR 09-MAR-2000; 2000US-0187999P.
 PR

PR 22-SEP-2000; 2000US-0234336P.
 XX (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIYV/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2002-434754/46.
 DR N-PSDB; ABK51853.
 XX
 PT New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX
 PS Claim 61; Fig 1; 180pp; English.
 XX
 CC The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGMR10 #1
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314
 RESULT 29
 AAU97152
 ID AAU97152 standard; protein; 352 AA.
 XX
 AC AAU97152;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation;
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;
 KW hyperproliferative disease; neurological disease; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002048786-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 09-FEB-2001; 2001US-00779879.
 XX

PR 09-FEB-2000; 2000US-0181258P.
 ER 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (ROSC/) ROSCHKE V.
 PA (LIYV/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2002-434754/46.
 DR N-PSDB; ABK51870.
 XX
 PT New nucleic acid encoding an antibody specific for the G-protein
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.
 PT inflammation.
 XX
 PS Disclosure; Page 165-166; 180pp; English.
 XX
 CC The present invention relates to the isolation of a novel human G-protein
 CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide
 CC sequences encoding it. The invention also describes antibodies that bind
 CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide
 CC sequences encoding the antibodies. The antibodies are useful for treating
 CC or preventing inflammation, defective or aberrant chemotaxis of immune
 CC cells and T-cell/antigen-presenting cell interactions, infections and
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral
 CC infections (especially early-stage human immune deficiency virus (HIV),
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions
 CC associated with aberrant or deficient expression of the CCR5 receptor or
 CC its ligands. The antibodies are also useful to determine CCR5 expression,
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other
 CC hyperproliferative diseases. The polynucleotide sequences encoding human
 CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the
 CC recombinant receptor, and in the treatment of a wide range of diseases
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The
 CC present sequence represents human G-protein chemokine receptor (CCR5)
 CC HDGMR10 #2
 XX
 SQ Sequence 352 AA;
 Query Match 100.0%; Score 95; DB 5; Length 352;
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314
 RESULT 30
 AAU52829
 ID AAU52829 standard; protein; 352 AA.
 XX
 AC AAU52829;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Human CCR5 Gln 55 variant.
 XX
 KW CCR5; CC chemokine receptor 5; human; HIV infection;
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
 KW drug screening; identification; variant.
 XX
 OS Homo sapiens.
 XX
 PN Location/Qualifiers
 XX Key
 FT Misc-difference 55 /note= "Glu replaces wild-type Leu; encoded by CTG"
 FT Misc-difference 58 /note= "Encoded by AGC"
 FT

```

XX WO200171346-A2.
XX
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009155.
XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-0190996P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813651.
XX PR 20-MAR-2001; 2001US-00813653.
XX PA (CONS-) CONSENSUS PHARM INC.
XX
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX
XX DR WPI; 2002-010610/01.
XX DR N-PSDB; ABA02318.
XX
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX
XX PS Example 3; Fig 4B; 50pp; English.
XX
XX CC The invention relates to a method for identifying a binding compound for
XX CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided method for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents a naturally occurring variant of human CCR5 in which
XX CC there is a glutamine, rather than a leucine, at position 55
XX
XX SQ Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNYLLVFFOK 18
XX Db 297 YAFVGEKFRNYLLVFFOK 314
XX
XX Search completed: March 4, 2004, 17:59:25
XX Job time : 43.7959 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 9.18367 Seconds

(without alignments)
188.535 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFNVLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 78:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	352	2 A43113	chemokine (C-C) re
2	79	83.2	360	2 J22443	chemokine (C-C) re
3	65	68.4	355	2 G02436	chemokine (C-C) re
4	64	67.4	359	2 I49341	MRP-1 alpha recept
5	63	66.3	355	2 J05067	G protein-coupled
6	62	65.3	383	2 S55594	G protein-coupled
7	61	64.2	359	2 J05068	G protein-coupled
8	60	63.2	355	2 A45177	chemokine (C-C) re
9	58	61.1	354	2 I58186	probable G protein
10	57	60.0	355	2 J04304	orphan G protein-c
11	57	60.0	360	2 A57160	chemokine (C-C) re
12	53	55.8	355	2 I49339	macrophage inflam
13	53	55.8	356	2 J49340	MRP-1 alpha recept
14	52	54.7	360	2 J04587	chemokine (C-C) re
15	52	54.7	378	2 B55735	lymphocyte-specifi
16	50	52.6	356	2 S42096	interleukin-8 rece
17	50	52.6	359	2 A48921	interleukin-8 rece
18	50	52.6	360	2 A53611	interleukin-8 rece
19	50	52.6	378	2 A56800	G protein-coupled
20	49	51.6	76	2 E95247	hypothetical prote
21	49	51.6	76	2 B98112	hypothetical prote
22	49	51.6	374	2 I38450	chemokine (C-C) re
23	48	50.5	367	2 J00349	interferon-inducib
24	47	49.5	358	2 A53752	interleukin-8 rece
25	47	49.5	378	2 A55735	G protein-coupled
26	46	48.4	354	2 A23669	interleukin-8 rece
27	46	48.4	355	2 J01231	interleukin-8 rece
28	45.5	47.9	377	2 B97185	glycosyltransferas
29	45	47.4	350	2 JN0621	G protein-coupled

30	45	47.4	359	2 J01104	angiotensin II rec
31	45	47.4	359	2 S44425	angiotensin II rec
32	45	47.4	359	2 J01194	angiotensin II rec
33	45	47.4	359	2 A48857	angiotensin II rec
34	45	47.4	359	2 A42656	angiotensin II rec
35	45	47.4	359	2 J01516	angiotensin II rec
36	45	47.4	359	2 S15403	angiotensin II rec
37	45	47.4	359	2 JH0621	angiotensin II rec
38	45	47.4	359	2 J02134	angiotensin II rec
39	44	46.3	358	2 G02670	IL8-related recept
40	44	46.3	375	2 J05069	G protein-coupled
41	43	45.3	119	2 C81207	hypothetical prote
42	43	45.3	259	2 E64514	hypothetical prote
43	43	45.3	293	2 T03883	hypothetical prote
44	43	45.3	297	2 C90270	sugar transport pr
45	43	45.3	333	2 I65989	G protein-coupled
46	43	45.3	350	2 S43497	opsin, 563nm - whi
47	43	45.3	362	2 A37783	opsin, red-sensiti
48	43	45.3	364	1 OOHUG	opsin, green-sensi
49	43	45.3	364	1 OOHUG	opsin, red-sensiti
50	43	45.3	1060	2 T30823	bumetanide sensiti
51	42.5	44.7	180	2 B90720	hypothetical prote
52	42.5	44.7	180	2 E85570	hypothetical prote
53	42.5	44.7	189	2 G64805	ybC protein - Esc
54	42.5	44.7	855	2 A45713	Env transmembrane
55	42	44.2	629	2 T34370	hypothetical prote
56	41	43.2	110	2 A6410	envelope protein (
57	41	43.2	110	2 D82455	hypothetical prote
58	41	43.2	203	2 T23282	hypothetical prote
59	41	43.2	326	2 G89835	conserved hypothet
60	41	43.2	350	2 A39445	interleukin-8 rece
61	41	43.2	365	2 B46191	cone visual pigmen
62	41	43.2	369	2 S33250	red visual pigment
63	41	43.2	375	2 J05509	G protein-coupled
64	41	43.2	397	2 E70317	hypothetical prote
65	41	43.2	632	2 E96723	hypothetical prote
66	41	43.2	919	2 S42842	TLG12.2 protein -
67	40.5	42.6	323	1 Q0BED3	HHRF3 protein - hu
68	40.5	42.6	927	2 T43110	lactacin 481/lacto
69	40	42.1	231	2 C69300	conserved hypothet
70	40	42.1	271	2 T18056	ATPase homolog A55
71	40	42.1	301	2 S56211	probable membrane
72	40	42.1	340	2 T44330	glycosyl transfera
73	40	42.1	349	2 C96738	unknown protein F3
74	40	42.1	354	2 T09353	G protein-coupled
75	40	42.1	371	2 J05498	G protein-coupled
76	40	42.1	421	2 T33811	hypothetical prote
77	40	42.1	425	2 T23560	hypothetical prote
78	40	42.1	543	2 T39345	probable metabolit
79	40	42.1	608	2 T18445	hypothetical prote
80	40	42.1	744	2 A70385	DNA gyrase A subun
81	40	42.1	834	2 E69380	methyl-accepting c
82	40	42.1	969	2 H69425	modification methy
83	40	42.1	1024	1 RNQBP	DNA-directed RNA p
84	40	42.1	1802	2 T71616	hypothetical prote
85	39.5	41.6	932	2 F84465	hypothetical prote
86	39	41.1	167	2 F81263	probable lipoprote
87	39	41.1	193	2 AG1988	hypothetical prote
88	39	41.1	211	2 G83718	DNA-binding protei
89	39	41.1	273	2 T51512	hypothetical prote
90	39	41.1	274	2 T41009	hypothetical prote
91	39	41.1	274	2 E91185	probable ATP-bindi
92	39	41.1	274	2 C86032	probable ATP-bindi
93	39	41.1	274	2 S47791	hypothetical prote
94	39	41.1	274	2 AI0979	probable exported
95	39	41.1	305	2 T43972	hypothetical prote
96	39	41.1	340	2 T30004	hypothetical prote
97	39	41.1	340	2 T09304	G protein-coupled
98	39	41.1	351	2 B42009	FWLP-related recep
99	39	41.1	391	2 T32714	hypothetical prote
100	39	41.1	507	2 T38653	trp-asp repeat pro

ALIGNMENTS

RESULT 1
A43113
chemokine (C-C) receptor 5 - human
N/Alternate names: C-C CKR-5; CCR5
C/Species: Homo sapiens (man)
C/Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C/Accession: A43113; S71808; A58834; A58832; G02653; A58833
R/Sanson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A/Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A/Reference number: A43113; MUID: 96241590; PMID: 8639485
A/Accession: A43113
A/Molecule type: mRNA
A/Residues: 1-352 <SAM1>
A/Cross-references: GB:X91492; NID: g1262810; PIDN: CAA62796.1; PID: g1262811
R/Sanson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liegnard, C.; Farber, C.M.; Saragosti
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.
Nature 382, 722-725, 1996
A/Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the *CCR5* gene
A/Reference number: S71808; MUID: 96345670; PMID: 8751444
A/Accession: S71808
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 182-206; 207-230 <SAM2>
A/Accession: A58834
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-184, 'TKDSHLCAGPAAACHGILLGNPKNSASVSK' <SAM3>
A/Cross-references: GB:X99393; NID: g1524062; PIDN: CAA67767.1; PID: g1524063
A/Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection
R/Combadiere, C.; Aluja, S.K.; Tiffany, H.L.; Murphy, P.M.
J. Leukoc. Biol. 60, 147-152, 1996
A/Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor
A/Reference number: A58832; MUID: 96295970; PMID: 8699119
A/Accession: A58832
A/Molecule type: mRNA
A/Residues: 1-352 <COM1>
A/Cross-references: GB:U57840; NID: g1502408; PIDN: AAB17071.1; PID: g1502409
A/Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R/Combadiere, C.
Submitted to the EMBL Data Library, May 1996
A/Reference number: H01541
A/Accession: G02653
A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-89, 'L', '91-352 <COM2>
A/Cross-references: EMBL:U57840
R/Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A/Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor
A/Reference number: A58833; MUID: 96291862; PMID: 8663314
A/Accession: A58833
A/Molecule type: mRNA
A/Residues: 1-352 <RAP>
A/Cross-references: GB:U54994; NID: g1457945; PIDN: AAC50598.1; PID: g1457946
C/Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine receptor and CXCR5
C/Genetics:
A/Status: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13
A/Cross-references: GDB:1230510; OMIM: 601373
A/Map position: 3p21-3p21
C/Function:
A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A/Note: probably acts to control granulocyte proliferation and differentiation
C/Superfamily: vertebrate rhodopsin
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F/32-56/Domain: transmembrane #status predicted <TM1>
F/67-87/Domain: transmembrane #status predicted <TM2>
F/103-124/Domain: transmembrane #status predicted <TM3>

F/142-166/Domain: transmembrane #status predicted <TM4>
F/193-218/Domain: transmembrane #status predicted <TM5>
F/236-257/Domain: transmembrane #status predicted <TM6>
F/285-300/Domain: transmembrane #status predicted <TM7>
F/20-269,101-178/Disulfide bonds: #status predicted
F/268/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted
F/340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 95; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
|||||

DB 297 YAFVGEKFRNLYLVFFQK 314
|||||

RESULT 2

JC2443
chemokine (C-C) receptor 2, splice form B - human
N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1
C/Species: Homo sapiens (man)
C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000
C/Accession: JC2443; I38463
R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994
A/Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1
A/Reference number: JC2443; MUID: 94324942; PMID: 8048929
A/Accession: JC2443
A/Molecule type: mRNA
A/Residues: 1-360 <YAM>
A/Cross-references: DDJ: D29884; NID: g531246; PIDN: BAA06253.1; PID: g531247
R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A/Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1
A/Reference number: A53477; MUID: 94195821; PMID: 8146186
A/Accession: I38463
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-360 <RES>
A/Cross-references: EMBL:U03905; NID: g472557; PIDN: AAA19120.1; PID: g472558
C/Genetics:
A/Status: GDB:CMKBR2
A/Cross-references: GDB: 337364; OMIM: 601267
A/Map position: 3p21-3p21
C/Superfamily: vertebrate rhodopsin
C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F/81-100/Domain: transmembrane #status predicted <TM1>
F/115-136/Domain: transmembrane #status predicted <TM2>
F/154-178/Domain: transmembrane #status predicted <TM3>
F/207-226/Domain: transmembrane #status predicted <TM4>
F/244-268/Domain: transmembrane #status predicted <TM5>
F/287-309/Domain: transmembrane #status predicted <TM6>
F/314/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/113-190/Disulfide bonds: #status predicted

Query Match 83.2%; Score 79; DB 2; Length 360;
Best Local Similarity 83.3%; Pred. No. 1.6e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
|||||

DB 305 YAFVGEKFRNLYLVFFQK 322
|||||

RESULT 3

G02436
chemokine (C-C) receptor 3 - human
N/Alternate names: C-C CKR-3
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000

C;Accession: G02436; A57237
 R;Ponath, P.D.
 Submitted to the EMBL Data Library, February 1996
 A;Reference number: H01272
 A;Accession: G02436
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <PON>
 A;Cross-references: EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477561
 R;Combadiere, C.; Ahuja, S.K.; Murphy, P.M.
 J. Biol. Chem. 270, 16491-16494, 1995
 A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
 A;Reference number: A57237; MUID:95348056; PMID:7622448
 A;Accession: A57237
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
 A;Cross-references: GB:U28694; NID:gl199579; PIDN:AAC50469.1; PID:gl199580
 A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
 C;Genetics:
 A;Gene: GDB:CMKBR3
 A;Cross-references: GDB:579624; OMIM:601268
 A;Map position: 3p21-3p21
 A;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-261/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;24-273, 106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 Query Match 68.4%; Score 65; DB 2; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0035;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YAFVGEKFRNVLVFFQK 18
 |||||:|:|:|:|:
 Db 301 YAFVGERFRKYLRFHFFR 318
 RESULT 4
 I49341
 MIP-1 alpha receptor like-2 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
 C;Accession: I49341
 R;Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine receptors.
 A;Reference number: I49339; MUID:95340546; PMID:7542241
 A;Accession: I49341
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-359 <RES>
 A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552
 C;Superfamily: vertebrate rhodopsin
 Query Match 67.4%; Score 64; DB 2; Length 359;
 Best Local Similarity 61.1%; Pred. No. 0.0052;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 YAFVGEKFRNVLVFFQK 18
 |||||:|:|:|:|:
 Db 305 YAFVGERFRKYLRFHFFR 322
 RESULT 5
 JC5067
 G protein-coupled receptor CKR-L1 - human

N;Alternate names: chemokine receptor-like protein TBR1; GPR-CY6
 C;Species: Homo sapiens (man)
 C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
 C;Accession: JC5067; G02776; G02387
 R;Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996
 A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like
 A;Reference number: JC5067; MUID:97040707; PMID:8886020
 A;Accession: JC5067
 A;Molecule type: DNA
 A;Residues: 1-355 <ZAB>
 A;Cross-references: EMBL:Z79782; NID:gl668735; PIDN:CAB02142.1; PID:gl668736
 R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: H01714
 A;Accession: G02776
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <NAP>
 A;Cross-references: EMBL:U62556; NID:gl468978; PID:gl468979
 R;Borner, I.I.
 submitted to the EMBL Data Library, January 1996
 A;Reference number: H01154
 A;Accession: G02387
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <BON>
 A;Cross-references: EMBL:U45983; NID:gl245056; PID:gl245057
 C;Comment: This protein belongs to the family of beta chemokine receptors.
 C;Genetics:
 A;Gene: GDB:CMKBR8; CMKBR2; TBR1; CKR-L1
 A;Cross-references: GDB:6053733; OMIM:601834
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein
 F;36-63/Domain: transmembrane #status predicted <TM1>
 F;73-94/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;200-222/Domain: transmembrane #status predicted <TM5>
 F;239-260/Domain: transmembrane #status predicted <TM6>
 F;281-304/Domain: transmembrane #status predicted <TM7>
 Query Match 66.3%; Score 63; DB 2; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0076;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YAFVGEKFRNVLVFFQK 18
 |||||:|:|:|:|:
 Db 300 YAFVGEKFKHLSEIFQK 317
 RESULT 6
 S55594
 G protein-coupled receptor E1 - equine herpesvirus 2
 C;Species: equine herpesvirus 2
 C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C;Accession: S55594
 R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
 J. Mol. Biol. 249, 520-528, 1995
 A;Title: The DNA sequence of equine herpesvirus 2.
 A;Reference number: S55594; MUID:95302501; PMID:7783207
 A;Accession: S55594
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-383 <TEL>
 A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor
 Query Match 65.3%; Score 62; DB 2; Length 383;
 Best Local Similarity 75.0%; Pred. No. 0.012;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      1 YAFVGEKFRNYLLVFF 16
      |||||:|||||:|||||
Db      340 YAFVGEKFRNYLLVFF 355

RESULT 7
JC5068
G protein-coupled receptor CXR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Guierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like 9
A:Reference number: JC5067; MUID:97040707; PMID:8886020
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:gl668738; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CXR-L3; GPR-CY4
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match      64.2%; Score 61; DB 2; Length 369;
Best Local Similarity 76.9%; Pred. No. 0.017;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLL 13
      |||||:|||||
Db      311 YAFVGEKFRNYLL 323

RESULT 8
A45177
chemokine (C-C) receptor 1 - human
N:Alternate names: C-C CXR-1; macrophage inflammatory protein-1-alpha receptor
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: A45177; J55671
R:Moote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-
A:Reference number: A45177; MUID:93161416; PMID:7679328
A:Accession: A45177
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-355 <NEO>
A:Cross-references: GB:ll10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A:Experimental source: HL60 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
R:Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
A:Reference number: I55671; MUID:93240122; PMID:7683036
A:Accession: I55671
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>
A:Cross-references: GB:ll10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C:Genetics:
A:Gene: GDB:CMKBR1; CMKBR-1

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A:Cross-references: GDB:138446; OMIM:601159
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-264/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:5/Binding site: carbohydrate (Agn) (covalent) #status predicted
F:24-273.106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match      63.2%; Score 60; DB 2; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.024;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||:|||||:|||||
Db      301 YAFVGEKFRNYLLVFFQK 318

RESULT 9
I58186
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: I58186
R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and
A:Reference number: I58186; MUID:94323113; PMID:8047298
A:Accession: I58186
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:Cross-references: EMBL:U04808; NID:g2558635; PIDN:AA87093.1; PID:g439861
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match      61.1%; Score 58; DB 2; Length 354;
Best Local Similarity 61.1%; Pred. No. 0.053;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||:|||||:|||||
Db      294 YAFVGEKFRNYLLVFFQK 311

RESULT 10
JC4304
orphan G protein-coupled receptor - human
N:Alternate names: V28 protein
C:Species: Homo sapiens (man)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C:Accession: JC4304
R:Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 293-299, 1995
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to
A:Reference number: JC4304; MUID:96011651; PMID:7590284
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A:Experimental source: peripheral blood mononuclear cell
C:Comment: This protein is a cell-surface receptor which recognizes extracellular signa
C:Comment: This protein is a key regulator of many immune and homeostatic responses, an
C:Genetics:
A:Gene: V28
A:Map position: 3pter-p21
C:Superfamily: vertebrate rhodopsin

```

A:Accession: I49339
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <RES>
A:Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
C:Superfamily: vertebrate rhodopsin

Query Match 55.8%; Score 53; DB 2; Length 355;
Best Local Similarity 55.6%; Pred. No. 0.37;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
| | | | | : | | | | : | | :
DB 301 YVFGKFRKYLQLQFOR 318

RESULT 13

I49340
MIP-1 alpha receptor like-1 - mouse
C:Species: Mus musculus (house mouse)
A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokins
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
A:Accession: I49340
A:Reference number: I49339; MUID:95340546; PMID:7542241
A:Accession: I49340
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-356 <RES>
A:Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550
C:Superfamily: vertebrate rhodopsin

Query Match 55.8%; Score 53; DB 2; Length 356;
Best Local Similarity 50.0%; Pred. No. 0.37; 5; Indels 0; Gaps 0;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
| | | | | : | | | | : | | :
DB 302 YVFGKFRKYLQLQFOR 319

RESULT 14

JC4587
chemokine (C-C) receptor 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C:Accession: JC4587
A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to RHOGEWERF, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A. Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A:Reference number: JC4587; MUID:96136324; PMID:8573157
A:Accession: JC4587
A:Molecule type: mRNA
A:Residues: 1-360 <HOO>
A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A:Experimental source: thymus
C:Genetics:
A:Gene: cc ckr-4
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus
F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:322/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 54.7%; Score 52; DB 2; Length 360;
Best Local Similarity 52.9%; Pred. No. 0.55;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 17
| | | | | : | | | | : | | :
DB 304 YFVLGEKFRKYLQLQFOR 320

RESULT 15

B55735
 Lymphocyte-specific G protein-coupled receptor EB11 - human
 N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
 C;Species: Homo sapiens (man)
 C;Accession: A48921; A53677; I49348; I55421; H48909; I53774
 C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
 R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
 Genomics 23, 643-650, 1994
 A;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
 A;Reference number: A55735; MUID:95154835; PMID:7851893
 A;Accession: B55735
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-378 <SCH>
 A;Cross-references: GB:131581; NID:9468319; PIDN:AAA74231.1; PID:9468320
 R;Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.
 submitted to the EMBL Data Library, February 1995
 A;Description: The expression of the chemokine receptor BLR2/EB11 is specifically transcribed in human lymphocytes.
 A;Reference number: S52443
 A;Accession: S52443
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 21-378 <HUR>
 A;Cross-references: EMBL:X84702
 C;Genetics:
 A;Gene: GDB:CMKBR7; EB11; BLR2; CCR7
 A;Cross-references: GDB:342065; OMIM:600242
 A;Map position: 17q12-17q21.2
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor

Query Match 54.78; Score 52; DB 2; Length 378;
 Best Local Similarity 58.8%; Pred. No. 0.57; Indels 5; Gaps 0;
 Matches 10; Conservative 2; Mismatches 5;

QY 1 YAFVGGKFRNYLLVFFQ 17
 |||:|||||:
 DB 326 YAFVGGKFRNDLFXLFK 342

RESULT 16

S42096
 Interleukin-8 receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
 C;Accession: S42096
 R;Gobi, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
 submitted to the EMBL Data Library, February 1994
 A;Description: Molecular cloning of the rat IL8 receptor.
 A;Reference number: S42096
 A;Accession: S42096
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-356 <GOB>
 A;Cross-references: EMBL:X77797
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.6%; Score 50; DB 2; Length 356;
 Best Local Similarity 69.2%; Pred. No. 1.2;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGGKFRNYLL 13
 |||:|||||:
 DB 310 YAFVGGKFRNYLL 322

RESULT 17

A48921
 Interleukin-8 receptor type B - mouse

N;Alternate names: G-protein coupled receptor Gpcrl6
 C;Species: Mus musculus (house mouse)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
 C;Accession: A48921; A53677; I49348; I55421; H48909; I53774
 R;Cerratti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993
 A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the A;Reference number: A48921; MUID:94117014; PMID:8288247
 A;Accession: A48921
 A;Molecule type: DNA
 A;Residues: 1-359 <CER>
 A;Cross-references: GB:123637; NID:9435093; PIDN:AAA9305.1; PID:9435094
 R;Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
 J. Biol. Chem. 269, 18263-18266, 1994
 A;Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding to A;Reference number: A53677; MUID:94308043; PMID:7518426
 A;Accession: A53677
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-359 <SUZ>
 A;Cross-references: GB:126549
 A;Note: sequence extracted from NCBI backbone (NCBIP:149812)
 R;Lee, J.; Cacalano, G.; Camarato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
 J. Immunol. 155, 2158-2164, 1995
 A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
 A;Reference number: I49348; MUID:95363183; PMID:7636264
 A;Accession: I49348
 A;Status: preliminary; translated from GB/EMBL/DBDJB
 A;Molecule type: DNA
 A;Residues: 1-359 <RES>
 A;Cross-references: EMBL:U31207; NID:9950174; PIDN:AAC52239.1; PID:9950175
 R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
 J. Biol. Chem. 269, 29355-29358, 1994
 A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression A;Reference number: I55421; MUID:95050766; PMID:7961903
 A;Accession: I55421
 A;Status: preliminary; translated from GB/EMBL/DBDJB
 A;Molecule type: DNA
 A;Residues: 1-359 <RE2>
 A;Cross-references: GB:131329; NID:9293665; PIDN:AAA62109.1; PID:9293666
 R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N. Genomics 18, 175-184, 1993
 A;Title: Identification, chromosomal location, and genome organization of mammalian G-p A;Reference number: A48909; MUID:94116980; PMID:8288218
 A;Accession: H48909
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 145-258 <WIL>
 A;Cross-references: GB:120337; NID:9438800; PIDN:AAA16853.1; PID:9438801
 R;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K. Gene 142, 297-300, 1994
 A;Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
 A;Reference number: I53774; MUID:94252584; PMID:8194768
 A;Accession: I53774
 A;Status: preliminary; translated from GB/EMBL/DBDJB
 A;Molecule type: mRNA
 A;Residues: 1-359 <RE3>
 A;Cross-references: GB:17630; NID:9493671; PIDN:BAA04536.1; PID:9493672
 C;Genetics:
 A;Gene: IL8rb
 A;Introns: #status absent
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
 F;84-106/Domain: transmembrane #status predicted <TM1>
 F;120-141/Domain: transmembrane #status predicted <TM3>
 F;163-182/Domain: transmembrane #status predicted <TM4>
 F;213-234/Domain: transmembrane #status predicted <TM5>
 F;251-271/Domain: transmembrane #status predicted <TM6>
 F;308-328/Domain: transmembrane #status predicted <TM7>

Query Match 52.6%; Score 50; DB 2; Length 359;
 Best Local Similarity 69.2%; Pred. No. 1.2;

A:Accession: A45680
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-378 <BUR>
A:Cross-references: GB:108176; NID:g183484; PID:g183485
A:Experimental source: B-lymphocytes
A>Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:127095)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.6%; Score 50; DB 2; Length 378;
Best Local Similarity 52.9%; Pred. No. 1.2; Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQ 17
||| : :
DB 326 YAFVGVKFRNDIFKLFK 342

RESULT 20
E95247
hypothetical protein SP2115 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95247
R:Rettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-76 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK76174.1; PID:g4973627; GSFPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2115

Query Match 51.6%; Score 49; DB 2; Length 76;
Best Local Similarity 62.5%; Pred. No. 0.37; Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFF 16
||| : :
DB 24 YAFVGVKFRNYLLVFF 39

RESULT 21
B98112
hypothetical protein spr1925 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: B98112
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
y, B.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B98112
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-76 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAL00727.1; PID:g15459622; GSFPDB:GN00174
C:Genetics:
A:Gene: spr1925

Query Match 51.6%; Score 49; DB 2; Length 76;
Best Local Similarity 62.5%; Pred. No. 0.37;

```
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFF 16
    |||||:|||||
Db 24 YAFGDFNYLAVF 39

RESULT 22
I38450
Chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 13-Aug-1999
C:Accession: I38450
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant pro
A:Reference number: A53477; MUID:94195821; PMID:8146186
C:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:9472556
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 51.6%; Score 49; DB 2; Length 374;
Best Local Similarity 90.0%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRN 10
    |||||:|
Db 305 YAFVGEKFRS 314

RESULT 23
JE0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C:Accession: JE0349
R:Tamari, M.; Tomimaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
A:Reference number: JE0349; MUID:99009219; PMID:9790904
C:Accession: JE0349
A:Molecule type: mRNA
A:Residues: 1-367 <TAM>
A:Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732
C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C:Superfamily: vertebrate rhodopsin

Query Match 50.5%; Score 48; DB 2; Length 367;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
    |||||:|
Db 317 YAFVGVKFRQMMMLFTR 334
```

```
RESULT 24
A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53752
R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarroz
J. Biol. Chem. 269, 12391-12394, 1994
A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A:Reference number: A53752; MUID:94230294; PMID:8175642
C:Accession: A53752
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <PRA>
A:Cross-references: GB:I24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 49.5%; Score 47; DB 2; Length 358;
Best Local Similarity 69.2%; Pred. No. 3.8;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
    |||||:|
Db 312 YAFVGEKFRNYLL 324

RESULT 25
A55735
G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor:
A:Reference number: A55735; MUID:95154835; PMID:7851893
C:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: GB:I31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 49.5%; Score 47; DB 2; Length 378;
Best Local Similarity 52.9%; Pred. No. 4;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQ 17
    |||||:|
Db 326 YAFVGEKFRSDLFKLFK 342

RESULT 26
A23669
interleukin-8 receptor, high affinity - rabbit
N:Alternate names: FMLP receptor
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: A23669
R:Thomas, K.M.; Pyun, H.Y.; Navarroz, J.
J. Biol. Chem. 265, 20061-20064, 1990
A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A:Reference number: A23669; MUID:91056034; PMID:1700779
C:Accession: A23669
A:Molecule type: mRNA
A:Residues: 1-354 <THO>
A:Cross-references: GB:M58021; NID:g165442; PIDN:AAA31377.1; PID:g165443
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil
```

```
Query Match      48.4%; Score 46; DB 2; Length 354;
Best Local Similarity 61.5%; Pred. No. 5.5;
Matches      8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVL 13
Db 309 YAFIQNFRNGFL 321

RESULT 27
JQ1231
interleukin-8 receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: JQ1231; A:46483
R:Beckmann, M.P.; Mungler, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, B.;
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A:Title: Molecular characterization of the interleukin-8 receptor.
A:Reference number: JQ1231; MUID:91378994; PMID:1898400
A:Accession: JQ1231
A:Molecule type: DNA
A:Residues: 1-355 <BEC>
A:Cross-references: GB:W74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
R:Lee, J.; Huang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A:Reference number: A46483; MUID:92148149; PMID:1737938
A:Accession: A46483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-355 <LEE>
A:Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A:Experimental source: neutrophils
A:Note: sequence extracted from NCBI backbone (NCBI:81526, NCBI:81530)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      48.4%; Score 46; DB 2; Length 355;
Best Local Similarity 61.5%; Pred. No. 5.5;
Matches      8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVL 13
Db 310 YAFIQNFRNGFL 322

RESULT 28
B97185
glycosyltransferase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: B97185
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97185
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK80269.1; PID:g15025320; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2313

Query Match      47.9%; Score 45.5; DB 2; Length 377;
Best Local Similarity 47.4%; Pred. No. 7.1;
Matches      9; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 3 FVG---EKFRNVLVFFQK 18
Db 227 FVGIEESFKNYITFFSK 245

Query Match      47.4%; Score 45; DB 2; Length 350;
Best Local Similarity 38.9%; Pred. No. 8;
Matches      7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 303 YFPMGTSPKYNIMKVAKK 320

RESULT 30
JC1104
angiotensin II receptor type 1 - human
N:Alternate names: angiotensin II receptor 1A
C:Species: Homo sapiens (man)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000
C:Accession: JC1104; JQ1402; JH0574; JH0267; A4014; S1893
R:Mauzy, C.A.; Huang, O.; Eglloff, A.M.; Wu, L.H.; Chung, F.Z.
Biochem. Biophys. Res. Commun. 186, 277-284, 1992
A:Title: Cloning, expression, and characterization of a gene encoding the human angiotensin
A:Reference number: JC1104; MUID:92337608; PMID:1378723
A:Accession: JC1104
A:Molecule type: DNA
A:Residues: 1-359 <MAU>
R:Furuta, H.; Guo, D.F.; Inagami, T.
Biochem. Biophys. Res. Commun. 183, 8-13, 1992
A:Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type
A:Reference number: JQ1402; MUID:92181475; PMID:1543512
A:Accession: JQ1402
A:Molecule type: DNA
A:Residues: 1-359 <FUR>
A:Cross-references: EMBL:Z11162; NID:g28709; PID:g28710
A:Experimental source: lymphocyte
R:Berghma, D.J.; Ellis, C.; Kumar, C.; Nurchalaganti, P.; Kersten, H.; Elshourbagy, N.; G
Biochem. Biophys. Res. Commun. 183, 989-995, 1992
A:Title: Cloning and characterization of a human angiotensin II type 1 receptor.
A:Reference number: JH0574; MUID:92231907; PMID:1567413
A:Accession: JH0574
A:Molecule type: mRNA
A:Residues: 1-359 <BER>
A:Cross-references: GB:M87290; NID:g178682; PIDN:AAA35535.1; PID:g178683
A:Experimental source: liver
R:Takayanagi, R.; Onnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Hajji, M.; Inagami, T.; F
Biochem. Biophys. Res. Commun. 183, 910-916, 1992
A:Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human ty
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A;Reference number: JH0267; MUID:92198490; PMID:1550596
A;Accession: JH0267
A;Molecule type: mRNA
A;Residues: 1-359 <YAK>
A;Experimental source: liver
R;Curnow, K.M.; Pascoe, L.; White, P.C.
Mol. Endocrinol. 6, 1113-1118, 1992
A;Title: Genetic analysis of the human type-1 angiotensin II receptor.
A;Reference number: A44014; MUID:92375105; PMID:1508224
A;Accession: A44014
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-359 <CUR>
A;Cross-references: GB:M93394; NID:gi78680; PID:gi78681
A;Note: sequence extracted from NCBI backbone (NCBIN:111831, NCBIIP:111833)
C;Genetics:
A;Gene: GDB:AGTR1
A;Cross-references: GDB:132359; OMIM:106165
A;Map position: 3q21-3q25
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein
F;30-53/Domain: transmembrane #status predicted <TM1>
F;65-90/Domain: transmembrane #status predicted <TM2>
F;103-124/Domain: transmembrane #status predicted <TM3>
F;145-167/Domain: transmembrane #status predicted <TM4>
F;194-216/Domain: transmembrane #status predicted <TM5>
F;241-264/Domain: transmembrane #status predicted <TM6>
F;281-305/Domain: transmembrane #status predicted <TM7>
F;4,176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.4%; Score 45; DB 2; Length 359;
Best Local Similarity 53.8%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
Db 302 YGFLGKKFRYFL 314

Search completed: March 4, 2004, 18:04:03
Job time : 10.1837 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 5.87755 Seconds
(without alignments)
159.465 Million cell updates/sec

Title: US-10-084-813-15
Perfect score: 95
Sequence: 1 YAFVGEKERNLLVFFQK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	95	100.0	352	1	CKR5_CERAE
2	95	100.0	352	1	CKR5_CERP
3	95	100.0	352	1	CKR5_CERTO
4	95	100.0	352	1	CKR5_GORGO
5	95	100.0	352	1	CKR5_HUMAN
6	95	100.0	352	1	CKR5_HYLE
7	95	100.0	352	1	CKR5_HYLM
8	95	100.0	352	1	CKR5_HYLSY
9	95	100.0	352	1	CKR5_MACMU
10	95	100.0	352	1	CKR5_PANTR
11	95	100.0	352	1	CKR5_PAPHA
12	95	100.0	352	1	CKR5_PONPY
13	95	100.0	352	1	CKR5_PYBHI
14	95	100.0	352	1	CKR5_PYGNE
15	95	100.0	352	1	CKR5_TRAFR
16	95	100.0	352	1	CKR5_TRAPH
17	85	89.5	354	1	CKR5_RAT
18	80	84.2	354	1	CKR5_MOUSE
19	78	82.1	373	1	CKR2_MOUSE
20	78	82.1	373	1	CKR2_RAT
21	76	80.0	360	1	CKR2_MACMU
22	65	68.4	355	1	CKR3_CERAE
23	65	68.4	355	1	CKR3_HUMAN
24	65	68.4	355	1	CKR3_MACMU
25	64	67.4	353	1	CKR8_MOUSE
26	64	67.4	359	1	CKR3_MOUSE
27	64	67.4	359	1	CKR3_RAT
28	63	66.3	355	1	CKR8_HUMAN
29	63	66.3	356	1	CKR8_MACMU
30	61	64.2	374	1	CKR6_HUMAN
31	60	63.2	355	1	CKR1_HUMAN
32	59	62.1	367	1	CKR6_MOUSE
33	58	61.1	354	1	C3X1_RAT

34	57	60.0	354	1	C3X1_MOUSE
35	57	60.0	355	1	C3X1_HUMAN
36	57	60.0	360	1	CKR4_HUMAN
37	56	58.9	355	1	CKR1_MACMU
38	55	57.9	358	1	CKR3_CAVPO
39	53	55.8	355	1	CKR1_MOUSE
40	53	55.8	356	1	CKR3_MOUSE
41	52	54.7	360	1	CKR4_MOUSE
42	52	54.7	378	1	CKR7_HUMAN
43	50	52.6	353	1	IL8B_MACMU
44	50	52.6	353	1	IL8B_PANTR
45	50	52.6	356	1	IL8B_CANFA
46	50	52.6	359	1	IL8B_MOUSE
47	50	52.6	359	1	IL8B_RAT
48	50	52.6	360	1	IL8B_HUMAN
49	49	51.6	322	1	CXCI_MOUSE
50	49	51.6	374	1	CKR2_HUMAN
51	47	49.5	358	1	IL8B_RABIT
52	47	49.5	367	1	CKR3_MOUSE
53	47	49.5	378	1	CKR7_MOUSE
54	47	49.5	781	1	APR2_SULTO
55	46	48.4	246	1	XPOT_MOUSE
56	46	48.4	355	1	IL8A_RABIT
57	46	48.4	360	1	IL8B_BOVIN
58	46	48.4	962	1	XPOT_HUMAN
59	45	47.4	350	1	CKRB_BOVIN
60	45	47.4	359	1	AG2R_BOVIN
61	45	47.4	359	1	AG2R_CANFA
62	45	47.4	359	1	AG2R_CAVPO
63	45	47.4	359	1	AG2R_HUMAN
64	45	47.4	359	1	AG2R_MERUN
65	45	47.4	359	1	AG2R_MOUSE
66	45	47.4	359	1	AG2R_PANTR
67	45	47.4	359	1	AG2R_PIG
68	45	47.4	359	1	AG2R_RABIT
69	45	47.4	359	1	AG2R_RAT
70	45	47.4	359	1	AG2R_SHEEP
71	45	47.4	359	1	AG2S_MOUSE
72	45	47.4	359	1	AG2S_RAT
73	44	46.3	350	1	CKRB_HUMAN
74	44	46.3	375	1	CML2_HUMAN
75	44	46.3	378	1	CML2_MOUSE
76	43	45.3	259	1	Y238_METJA
77	43	45.3	333	1	CXCI_HUMAN
78	43	45.3	349	1	IL8A_RAT
79	43	45.3	350	1	OPSL_CALJA
80	43	45.3	357	1	CKR9_HUMAN
81	43	45.3	359	1	OPSG_RAT
82	43	45.3	362	1	OPSR_CHICK
83	43	45.3	364	1	OPSG_CAVPO
84	43	45.3	364	1	OPSG_HUMAN
85	43	45.3	364	1	OPSG_RABIT
86	43	45.3	364	1	OPSG_SCICA
87	43	45.3	364	1	OPSR_CAPHI
88	43	45.3	364	1	OPSR_HUMAN
89	43	45.3	369	1	CKR9_MOUSE
90	43	45.3	384	1	CKD6_HUMAN
91	43	45.3	1060	1	NKCL_MANSE
92	42.5	44.7	189	1	YBFC_ECOLI
93	42	44.2	303	1	HTFX_FUSNN
94	42	44.2	353	1	IL8B_GORGO
95	42	44.2	359	1	OPSG_MOUSE
96	42	44.2	361	1	P2V4_MOUSE
97	42	44.2	361	1	P2V4_RAT
98	42	44.2	629	1	GAP1_CAEEL
99	41	43.2	350	1	IL8A_GORGO
100	41	43.2	350	1	IL8A_HUMAN

ALIGNMENTS

RESULT 1

CKR5_CERAE
ID -CKR5 CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX MEDLINE=98001387; PubMed=9143222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; U83324; AAC51795.1; -;
CC EMBL; U83325; AAC51796.1; -;
CC EMBL; AB015944; BAA31328.1; -;
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm1.1;
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G PROTEIN RECF F1.1; 1.
CC PROSITE; PS0262; G PROTEIN RECF F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
CC Polymorphism.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 199 218 5 (POTENTIAL).
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 236 260 6 (POTENTIAL).
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 278 301 7 (POTENTIAL).
CC DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 353 378 BY SIMILARITY.
CC DISULFID 101 178
CC FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
CC FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

FT VARIANT 14 14 N -> Y.
FT VARIANT 352 352 P -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;
Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNLLVFFQK 18
|||||
DB 297 YAFVGEKFRNLLVFFQK 314
|||||
RESULT 2
CKR5_CERPY
ID -CKR5 CERPY STANDARD; PRT; 352 AA.
AC Q9TV42;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=100;
RX MEDLINE=9933215; PubMed=10408730;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
carrier status in African nonhuman primates.";
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL; AF035222; AAD44015.1; -;
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm1.1;
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G PROTEIN RECF F1.1; 1.
CC PROSITE; PS0262; G PROTEIN RECF F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 199 218 5 (POTENTIAL).
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 236 260 6 (POTENTIAL).
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 278 301 7 (POTENTIAL).

```

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLVFFQK 18
DB 297 YAFVGEKFRNYLVFFQK 314

RESULT 3
ID CCR5_CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecidae;
OX NCBI_TaxID=9531;
[1]

SEQUENCE FROM N.A.
RP STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary HIV isolates use the CCR5 coreceptor from sooty mangabeys
naturally infected in west Africa: a comparison of coreceptor usage
of primary HIV-1, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 2; 1.
CC PROSITE; PS00262; G PROTEIN RECEPTOR FL 3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).

```

```

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 3 3 Y -> G (IN ISOLATE 087).
FT VARIANT 25 25 V -> G (IN ISOLATE 079).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLVFFQK 18
DB 297 YAFVGEKFRNYLVFFQK 314

RESULT 4
ID CCR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_TaxID=9595;
[1]

SEQUENCE FROM N.A.
RP MEDLINE=97285687; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005659; AAB62553.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.

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DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09; Indels 0;
 Matches 18; Conservative 0; Mismatches 0; Caps 0;

QY 1 YAFVGEKFNLYLVFFQK 18
 |||||
 DB 297 YAFVGEKFNLYLVFFQK 314

RESULT 5
 CKR5 HUMAN STANDARD; PRT; 352 AA.
 AC P51681; O14692; O14693; O14696; O14697; O14698; O14699;
 AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
 AC O14708; O15538; Q9UP84;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)
 DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
 GN CCR5 OR CMKBR5.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96241590; PubMed=8639485;
 RA Samson M., Jabbe O., Mollereau C., Vaessart G., Parmentier M.;
 RT "Molecular cloning and functional expression of a new human
 RT CC chemokine receptor gene";
 RL Biochemistry 35:3362-3367(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96291862; PubMed=8663314;
 RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
 RT "Molecular cloning and functional characterization of a novel human
 RT CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha";
 RL J. Biol. Chem. 271:17161-17166(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96295970; PubMed=8699119;
 RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
 RT "Cloning and functional expression of CC CKR5, a human monocyte CC
 RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
 RT RANTES";
 RL J. Leukoc. Biol. 60:147-152(1996).
 RN [4]

RP SEQUENCE FROM N.A.
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
 RA Khan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
 RA Guoj L., Ia Bastide M., Kaplan N., Greco T., Touchman J.,
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
 RA Matanabe M., Doggett N., Garcia D., Sagripanti J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98001387; PubMed=9343222;
 RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses";
 RL J. Virol. 71:8642-8656(1997).
 RN [6]
 RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049523; PubMed=9388201;
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
 RT with 5'-end heterogeneity, dual promoter usage, and evidence for
 RT polymorphisms within the regulatory regions and noncoding exons";
 RL J. Biol. Chem. 272:30662-30671(1997).
 RN [8]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,
 RA Debre P.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=98260017; PubMed=8649511;
 RA Deng H., Liu R., Elmeyer W., Choe S., Unutmaz D., Burkhardt M.,
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 RT HIV-1";
 RL Nature 381:661-666(1996).
 RN [11]
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RX MEDLINE=98260018; PubMed=8649512;
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 RT CC-CKR-5";
 RL Nature 381:667-673(1996).
 RN [12]
 RP SULFATION.
 RX MEDLINE=99189752; PubMed=10089882;
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 RT entry";
 RL Cell 96:667-676(1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and rantes and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or

GO; GO:0007186; P-G-protein coupled receptor protein signalin. . . ; TAS.
GO; GO:006954; P-inflammatory response; TAS.
GO; GO:0007125; P-invasive growth; TAS.
GO; GO:0007023; P-phosphatidylinositol-4,5-bisphosphate hydro. . . ; TAS.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODPSN
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 31 58 1 (POTENTIAL).
FT FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 69 89 2 (POTENTIAL).
FT FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 103 124 3 (POTENTIAL).

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||||
DB 297 YAFVGEKFRNYLLVFFQK 314
|||||

RESULT 6

CKR5_HYLLE STANDARD; PRT; 352 AA.

ID CKR5_HYLLE
AC 097883;
DT 30-MAY-2000 (Rel. 39, Created)
DD 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DS C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Hylobates leucogynus (White-cheeked gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
NCBI_TaxID=61853;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99416436; PubMed=10486970;
RX Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RA "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RT Mol. Biol. Evol. 16:1145-1154(1999).
RL CC
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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or send an email to license@isb-sib.ch)

EMBL; AF075451; AD19863.1; --
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT FT TRANSMEM 31 58 1 (POTENTIAL).
FT FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 7
 CCR5_HYLM
 ID CCR5_HYLM STANDARD; PRT; 352 AA.
 AC Q95NC0;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Hylobates moloch (silvery gibbon).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini, Hylobatidae; Hylobates.
 OX NCBI_TaxID=81572;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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CC EMBL; AF177899; AAK43382.1; -;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm.1.1
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.
 CC PROSITE; PS0262; G PROTEIN RECEPTOR F1.2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40436 MW; 5623CA98340CF274 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
 |||||
 Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 8
 CCR5_HYLSY
 ID CCR5_HYLSY STANDARD; PRT; 352 AA.
 AC Q95NC5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).
 GN CCR5 OR CCR5.
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini, Hylobatidae; Hylobates.
 OX NCBI_TaxID=9590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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CC EMBL; AF177884; AAK43367.1; -;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm.1.1
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.
 CC PROSITE; PS0262; G PROTEIN RECEPTOR F1.2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).

```

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

```

RESULT 9

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ID CKR5_MACMU STANDARD; PRT; 352 AA.
AC P79436; 002746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CKR5 OR CXCR5.
OS Macaca mulatta (Rhesus macaque).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239.";
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RA J. Virol. 71:2705-2714(1997).
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CKR5 as a coreceptor for entry.";
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Pelper S.C., Parmentier M., Broder C.C., Doms R.W.;

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RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U77672; AAC51109.1; -
CC EMBL; U73739; AAC51158.1; -
CC EMBL; U96762; AAC34132.1; -
CC EMBL; AF005660; AB62554.1; -
CC EMBL; AF005661; AB62555.1; -
CC EMBL; AF005662; AB62556.1; -
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 10
CKR5_PANTR
ID CKR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; 002778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).

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GN CCR5 OR CMKRS5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98022612; PubMed=9359654;
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97426118; PubMed=9282822;
 RA Zacharova V., Zachar V., Gouatin A.S.;
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
 RT HIV type 1 host.";
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98090115; PubMed=9430250;
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
 RT "Chimpanzee CCR4 and CCR5 act as coreceptors for HIV type 1.";
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX Zhang Y., Ryder O.A., Zhang Y.;
 RT "sequence comparison of the CCR5 gene in primates and primate
 RT phylogeny.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF005663; AAB62557.1; -
 CC EMBL; U94329; AAB58446.1; -
 CC EMBL; AF011542; AAB65742.1; -
 CC EMBL; U97666; AAC31670.1; -
 CC EMBL; AF011540; AAB65740.1; -
 CC EMBL; U89797; AAC03717.1; -
 CC EMBL; AF17894; AAK43377.1; -
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 123 123 T -> S (IN REF. 1).
 SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B0FE34C CRC64;
 Query Match 100.0%; Score 95; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YAFVGEKFRNLLVFFQK 18
 Db 297 YAFVGEKFRNLLVFFQK 314
 RESULT 11
 CCR5 PAPA
 ID CCR5_PAPA STANDARD; PRT; 352 AA.
 AC P56441;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR5).
 GN CCR5 OR CMKRS5.
 OS Papio hamadryas (Hamadryas baboon), and
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Papio.
 OX NCBI_TaxID=9557, 9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX SPECIES=P.hamadryas;
 RX MEDLINE=97268687; PubMed=9108095;
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
 RT "Differential utilization of CCR5 by macrophage and T cell tropic
 RT simian immunodeficiency virus strains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX SPECIES=P.hamadryas;
 RX MEDLINE=99210133; PubMed=10195758;
 RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
 RT "Species-specific changes in the CCR5 gene from African and Asian
 RT nonhuman primates.";
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX SPECIES=P.anubis;
 RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF005658; AAB62552.1; -
 CC EMBL; AF105287; AAD20556.1; -
 CC EMBL; AF105288; AAD20557.1; -
 CC EMBL; AF105289; AAD20558.1; -
 CC EMBL; AF105290; AAD20559.1; -
 CC EMBL; AF023452; AAC63830.1; -
 CC InterPro; IPR000276; GPCR_Rhodopsin.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 31 58
 CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 69 89
 CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 103 124
 CC FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 142 166
 CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 199 218
 CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 236 260
 CC FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 278 301
 CC FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 101 178 BY SIMILARITY.
 CC FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 CC FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 CC FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 CC FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 352 AA; 40489 MW; 5E15049BA1F5882 CRC64;
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 CC Query Match 100.0%; Score 95; DB 1; Length 352;
 CC Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 YAFVGEKFNLYLVFFQK 18
 CC |||||
 CC Db 297 YAFVGEKFNLYLVFFQK 314
 CC
 CC RESULT 12
 CC CKR5_PONPY
 CC ID CKR5_PONPY STANDARD; PRT; 352 AA.
 CC AC 097881;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 CC GN CCR5 OR CKR5.
 CC OS Pongo pygmaeus (Orangutan).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 CC ON NCBI_TaxID=9600;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.

RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154 (1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF075446; AAD19858.1; -
 CC InterPro; IPR000276; GPCR_Rhodopsin.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
 CC PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 CC FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 31 58
 CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 69 89
 CC FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 103 124
 CC FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 142 166
 CC FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 199 218
 CC FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 236 260
 CC FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 278 301
 CC FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 CC FT DISULFID 101 178 BY SIMILARITY.
 CC FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 CC FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 CC FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
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 CC Query Match 100.0%; Score 95; DB 1; Length 352;
 CC Best Local Similarity 100.0%; Pred. No. 6.9e-09;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 YAFVGEKFNLYLVFFQK 18
 CC |||||
 CC Db 297 YAFVGEKFNLYLVFFQK 314
 CC
 CC RESULT 13
 CC CKR5_PYGBI
 CC ID CKR5_PYGBI STANDARD; PRT; 352 AA.
 CC AC 097880;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 CC GN CCR5 OR CKR5.
 CC OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 CC OC Pygathrix.
 CC ON NCBI_TaxID=61621;
 CC RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE:99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154 (1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AF075445; AAD19857.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm 1; 1.
CC PRINTS: PR00237; GPCRHHODOPSN.
CC PROSITE: PS00237; G PROTEIN RECP F1.1; 1.
CC PROSITE: PS00262; G PROTEIN RECP F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC
CC DOMAIN 1 30
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 59 68
CC TRANSMEM 69 89
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 90 102
CC TRANSMEM 103 124
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 125 141
CC TRANSMEM 142 166
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 167 198
CC TRANSMEM 199 218
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 219 235
CC TRANSMEM 236 260
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 261 277
CC TRANSMEM 278 301
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 302 323
CC BY SIMILARITY.
CC DISULFID 101 178
CC SULFATION (BY SIMILARITY).
CC MOD_RES 3 3
CC SULFATION (BY SIMILARITY).
CC MOD_RES 10 10
CC SULFATION (BY SIMILARITY).
CC MOD_RES 14 14
CC SULFATION (BY SIMILARITY).
CC MOD_RES 15 15
CC SULFATION (BY SIMILARITY).
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CC SEQUENCE 352 AA; 40585 MW; 4366f142730f938f CRC64;
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Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 14
CCR5_PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMBKRS.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=54133;

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RN SEQUENCE FROM N.A.
RP MEDLINE:99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154 (1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: AF075448; AAD19860.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm 1; 1.
CC PRINTS: PR00237; GPCRHHODOPSN.
CC PROSITE: PS00237; G PROTEIN RECP F1.1; 1.
CC PROSITE: PS00262; G PROTEIN RECP F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC
CC DOMAIN 1 30
CC EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 59 68
CC TRANSMEM 69 89
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 90 102
CC TRANSMEM 103 124
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 125 141
CC TRANSMEM 142 166
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 167 198
CC TRANSMEM 199 218
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 219 235
CC TRANSMEM 236 260
CC EXTRACELLULAR (POTENTIAL).
CC DOMAIN 261 277
CC TRANSMEM 278 301
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 302 352
CC BY SIMILARITY.
CC DISULFID 101 178
CC SULFATION (BY SIMILARITY).
CC MOD_RES 3 3
CC SULFATION (BY SIMILARITY).
CC MOD_RES 10 10
CC SULFATION (BY SIMILARITY).
CC MOD_RES 14 14
CC SULFATION (BY SIMILARITY).
CC MOD_RES 15 15
CC SULFATION (BY SIMILARITY).
CC
CC SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3861 CRC64;
Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 297 YAFVGEKFRNYLLVFFQK 314

RESULT 15
CCR5_TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMBKRS.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Trachypithecus.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=98334064; PubMed=9670989;
RA Spieiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA Berger M., Gebicke-Haerter P.J.;
RT "Cloning of rat HIV-1-chemokine coreceptor CXCR5 from microglia and
RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RL J. Neurosci. Res. 53:16-28(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis";
RL J. Neuroimmunol. 86:1-12(1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
DR EMBL; Y12009; CAA72737.1; -;
DR EMBL; U77350; AAC03243.1; -;
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPSIN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 2; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 60
FT DOMAIN 61 70
FT TRANSMEM 71 91
FT DOMAIN 92 104
FT TRANSMEM 105 126
FT DOMAIN 127 143
FT TRANSMEM 144 168
FT DOMAIN 169 200
FT TRANSMEM 201 220
FT DOMAIN 221 237
FT TRANSMEM 238 262
FT DOMAIN 263 279
FT TRANSMEM 280 303
FT DOMAIN 304 354
FT DISULFD 103 180
FT CAROHYD 270 270
SQ SEQUENCE 354 AA; 41030 MW; 77ED368AA4C868D CRC64;
Query Match 89.5%; Score 85; DB 1; Length 354;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

Db 299 YAFVGEKFRNLLVFFQK 316

RESULT 18
CKR5_MOUSE

ID AC
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN CKR5 OR CXCR5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Spleen;
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Gosling J., Montecarlo F.S., Luisi A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT 1alpha receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9";
RL J. Biol. Chem. 271:7551-7558(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96278910; PubMed=8662890;
RA Meyer A., Coyte A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RX Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RX MEDLINE=98001387; PubMed=9343222;
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses";
RL J. Virol. 71:8642-8656(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=97404635; PubMed=9261347;
RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
RT "Two distinct CCR5 domains can mediate coreceptor usage by human
RT immunodeficiency virus type 1";
RL J. Virol. 71:6305-6314(1997).
RN [6]
RP SEQUENCE FROM N.A.
RC Guo B., Kuno K., Harada A., Matsushima K.;
RX Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC

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CC EMBL; U47035; AAC52453.1; --
DR EMBL; X94151; CAA63867.1; --
DR EMBL; U68565; AAB37273.1; --
DR EMBL; U83327; AAC53386.1; --
DR EMBL; AF022990; AAC53389.1; --
DR EMBL; AF019772; AAB71183.1; --
DR EMBL; D83648; BAA12024.1; --
DR MGJ; MGJ:107182; Ccr5.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR GO; GO:0006952; P:defense response; IMP.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHOOPS.
DR PROSITE; PS00237; G PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
FT DOMAIN 1 32
FT TRANSEM 33 60
FT DOMAIN 61 70
FT TRANSEM 71 91
FT DOMAIN 92 104
FT TRANSEM 105 126
FT DOMAIN 127 143
FT TRANSEM 144 168
FT DOMAIN 169 200
FT TRANSEM 201 220
FT DOMAIN 221 237
FT TRANSEM 238 262
FT DOMAIN 263 279
FT TRANSEM 280 303
FT DOMAIN 304 354
FT DISULFID 103 180
FT CARBOHYD 270 270
FT VARIANT 11 11
FT VARIANT 62 62
FT VARIANT 66 66
FT VARIANT 97 97
FT VARIANT 109 109
FT VARIANT 156 156
FT VARIANT 160 160
FT VARIANT 185 185
FT VARIANT 213 213
FT VARIANT 318 318
FT VARIANT 337 337
FT CONFLICT 3 3 F -> L (IN REF. 2).
FT CONFLICT 80 80 L -> F (IN REF. 2).
FT CONFLICT 145 145 N -> Y (IN REF. 5).
FT CONFLICT 190 190 H -> Y (IN REF. 3).
FT CONFLICT 208 208 P -> S (IN REF. 1).
SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;

Query Match 84.2%; Score 80; DB 1; Length 354;
Best Local Similarity 83.3%; Pred. No. 2.7e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
Db 299 YAFVGEKFRNLYLVFFQK 316

RESULT 19
ID_CKR2_MOUSE STANDARD; PRT; 373 AA.
AC P51683; Q61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (JE/FIC receptor) (MCP-1 receptor).
DE CCR2 OR CMKR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP MEDLINE=96205938; PubMed=8631787;
RX Boring L., Gosling J., Montecarlo F.S., Luis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
chemoattractant protein 1) and murine macrophage inflammatory protein
1alpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9.";
RL J. Biol. Chem. 271:7551-7558(1996).
RN SEQUENCE FROM N.A.
RP STRAIN=BALE/C;
RX MEDLINE=96216064; PubMed=8662823;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
the C-C chemokines JE and FIC.";
RL J. Biol. Chem. 271:11603-11606(1996).
RN SEQUENCE FROM N.A.
RP MEDLINE=97026720; PubMed=8872898;
RX Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA Post T.W., Gerard C., Dorf M.E.;
RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
transcriptase-polymerase chain reaction does not detect mRNA for the
KC or new MCP-1 receptor.";
RL J. Neurosci. Res. 45:382-391(1996).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
chemokines. Transduces a signal by increasing the intracellular
calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
but not in nonhematopoietic cell lines.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
DR EMBL; U47035; AAC52453.1; --
DR EMBL; U51717; AAC52557.1; --
DR EMBL; U56819; AAC52784.1; --
DR MGJ; MGJ:106185; Ccr2.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR GO; GO:0019955; P:cytokine binding; IPI.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
DR GO; GO:0030097; P:hemopoiesis; IMP.
DR GO; GO:0006959; P:humoral immune response; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0030334; P:regulation of cell migration; IMP.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHOOPS.
DR PROSITE; PS00237; G PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55
FT TRANSEM 56 83
FT DOMAIN 84 93
FT TRANSEM 94 114
FT DOMAIN 115 127
FT TRANSEM 128 149
FT DOMAIN 150 166
FT TRANSEM 167 191
FT DOMAIN 192 219
FT TRANSEM 220 239
FT DOMAIN 240 256
FT TRANSEM 240 256

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FT TRANSMEM 257 281 6 (POTENTIAL).
 FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 299 322 7 (POTENTIAL).
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 FT CONFLICT 39 39 Y -> H (IN REF. 1).
 FT CONFLICT 184 184 A -> G (IN REF. 1).
 FT CONFLICT 264 264 V -> G (IN REF. 1).
 SQ SEQUENCE 373 AA; 42782 MW; PA012C10F4C9325A CRC64;

Query Match 82.1%; Score 78; DB 1; Length 373;
 Best Local Similarity 77.8%; Pred. No. 6.4e-06;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFNLYLVFFOK 18
 ||||| ||| :|||
 Db 318 YAFVGEKFNLYLVFFOK 335

RESULT 20

CKR2 RAT
 ID CKR2 RAT STANDARD; PRT; 373 AA.
 AC 055193;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).
 GN CKR2 OR CMKR2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98318173; PubMed=9655467;
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
 defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
 RT "Chemokine receptor expression in cultured glia and rat experimental
 allergic encephalomyelitis";
 RL J. Neuroimmunol. 86:1-12(1998).
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (PIC) and MCP-5
 chemokines. Transduces a signal by increasing the intracellular
 calcium ions level (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
 macrophages.
 CC -!- INDUCTION: In animals in which experimental allergic
 encephalomyelitis (EAE) has been induced.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC -----

CC EMBL; U77349; AAC03242.1; -;
 CC InterPro; IPR000276; GPCR_Rhodopn.
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1.1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL2.1; 1.
 CC G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 61 81 POTENTIAL.
 FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 92 112 POTENTIAL.
 FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 POTENTIAL.
 FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 171 191 POTENTIAL.
 FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 221 241 POTENTIAL.
 FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 257 277 POTENTIAL.
 FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 302 322 POTENTIAL.
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 126 203 BY SIMILARITY.
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 82.1%; Score 78; DB 1; Length 373;
 Best Local Similarity 77.8%; Pred. No. 6.4e-06;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFNLYLVFFOK 18
 ||||| ||| :|||
 Db 318 YAFVGEKFNLYLVFFOK 335

RESULT 21

CKR2 MACMU
 ID CKR2 MACMU STANDARD; PRT; 360 AA.
 AC 018793;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
 GN (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
 GN CKR2 OR CMKR2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 receptors";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
 CC Transduces a signal by increasing the intracellular calcium ions
 CC level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Name=B;
 CC Name=A;
 CC IsoId=O18793-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=O18793-2; Sequence=Not described;
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC -----

CC EMBL; AF013958; AAD11572.1; -;
 CC InterPro; IPR000276; GPCR_Rhodopn.
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODPSN
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1.1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL2.1; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 CC Alternative splicing.
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 43 70 1 (POTENTIAL).
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).

FT TRANSNM 81 100 2 (POTENTIAL).
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
 FT TRANSNM 115 136 3 (POTENTIAL).
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSNM 154 178 4 (POTENTIAL).
 FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
 FT TRANSNM 207 226 5 (POTENTIAL).
 FT DOMAIN 227 243 6 (POTENTIAL).
 FT TRANSNM 244 268 7 (POTENTIAL).
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
 FT TRANSNM 286 309 7 (POTENTIAL).
 FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD RES 26 26 SULFATION (BY SIMILARITY).
 FT DISULFID 113 190 BY SIMILARITY.
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 80.0%; Score 76; DB 1; Length 360;
 Best Local Similarity 77.8%; Pred. No. 1.4e-05;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFPQK 18
 DB 305 YAFVGEKFRNVLVFPQK 322

RESULT 22

ID_CKR3_CERAE STANDARD; PRT; 355 AA.
 AC P56452;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
 DE (CCR3).
 GN CCR3 OR CMKBR3.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sol N., Treboute C., Gomas E., Ferchal F., Alison M.;
 RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin.
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; Y13775; CAA74106.1;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS0262; G PROTEIN RECP F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSNM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSNM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSNM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT

FT TRANSNM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSNM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSNM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSNM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 SQ SEQUENCE 355 AA; 40830 MW; 44F7A5EFEB978FF CRC64;

Query Match 68.4%; Score 65; DB 1; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0011;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFPQK 18
 DB 301 YAFVGEKFRNVLVFPQK 318

RESULT 23

CKR3_HUMAN STANDARD; PRT; 355 AA.
 ID_CKR3_HUMAN STANDARD; PRT; 355 AA.
 AC P51677; Q15748; Q86WD2; Q9ULY8;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
 DE (CCR3) (Eosinophil eotaxin receptor).
 GN CCR3 OR CMKBR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Monocytes;
 RX MEDLINE=95348056; PubMed=7622448;
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RA "Cloning and functional expression of a human eosinophil CC chemokine
 RT receptor.";
 RL J. Biol. Chem. 270:16491-16494 (1995).
 RN [2]
 RP ERRATUM.
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RL J. Biol. Chem. 270:30235-30235 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96235044; PubMed=8642344;
 RA Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L.,
 RA Sirotina A., Springer M.S.;
 RA "Cloning, expression, and characterization of the human eosinophil
 RT eotaxin receptor.";
 RL J. Exp. Med. 183:2349-2354 (1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96281895; PubMed=8676064;
 RA Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,
 RA Newman W., Gerard C., Mackay C.R.;
 RA "Molecular cloning and characterization of a human eotaxin receptor
 RT expressed selectively on eosinophils.";
 RL J. Exp. Med. 183:2737-2748 (1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1
 RT in exposed uninfected individuals homozygous for CCR5 32bp deletion.";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A., AND VARIANT SER-218.
 RX MEDLINE=21040311; PubMed=11196669;
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
 RA Hirai K., Tokunaga K.;

RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
 RL Genes Immun. 1:97-104(1999).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22074933; PubMed=12079287;
 RA Vijh S., Dayhoff D.B., Wang C.E., Imam Z., Ehrenberg P.K.,
 RA Michael N.L.;
 RT "Transcription regulation of human chemokine receptor CCR3: evidence
 RT for a rare TATA-less promoter structure conserved between Drosophila
 RT and humans";
 RL Genomics 80:86-95(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Lung, and Testis;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Lomellano N.A., Peters G.J., Abranson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
 CC eotaxin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently
 CC transduces a signal by increasing the intracellular calcium ions
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: In eosinophils as well as trace amounts in
 CC neutrophils and monocytes.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; U28694; AAC50469.1; -;
 DR EMBL; U51241; AAB16811.1; -;
 DR EMBL; U45727; AAB09726.1; -;
 DR EMBL; AF026535; AAB82589.1; -;
 DR EMBL; AB023887; AAB86964.1; -;
 DR EMBL; AF247361; AAL85154.1; -;
 DR EMBL; AY221092; AAO65970.2; -;
 DR EMBL; BC033514; AAB33514.1; -;
 DR EMBL; G02436; G02436.
 DR Genew; HGNC:1604; CCR3.
 DR MIM; 601268; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0006368; P:cellular defense response; TAS.

DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0007188; P:G-protein signaling, coupled to GMP nucleos. .; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0007125; P:invasive growth; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR00237; GPCRHOOPSN
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Polymorphism.
 KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 34
 FT TRANSMEM 35 62 1 (POTENTIAL).
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 204 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 FT VARIANT 218 218 C->S (polymorphism found in about 7% of
 FT the population; may show reduced
 FT activity).
 FT CONFLICT 276 276 S->T (IN REF. 4 AND 5).
 FT SEQUENCE 355 AA; 41043 MW; B95DCD7A6C643874 CRC64;
 Query Match 68.4%; Score 65; DB 1; Length 355;
 Best Local Similarity 66.7%; Pred. No. 0.0011;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 YAFVGEKPNVLLVFFOK 18
 |||||:|||||:
 DB 301 YAFVGEKPNVLLVFFOK 318
 RESULT 24
 CCR3 MACMU STANDARD; PRT; 355 AA.
 ID CCR3 MACMU STANDARD; PRT; 355 AA.
 AC F56483;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 3 (C-C CCR-3) (CCR-3) (CCR3)
 DE (CCR3).
 GN CCR3 OR CCR3R3.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OC NCBI_TaxID=9544;
 OX [1]_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors";
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98118446; PubMed=9454694;
 RA Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;
 RT "The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
 RT for HIV-2, but not for HIV-1";
 RL Virology 240:213-220(1998).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,


```

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RT Gerard C.;
RA "Molecular characterization of two murine eosinophil beta chemokine
RT receptors.";
RL J. Immunol. 155:5299-5305 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501 (1995).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
CC amounts in leukocytes.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; U29677; AAA6118.1; -.
DR EMBL; U28406; AAA89155.1; -.
DR MGD; MGI:104616; Ccr3.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006935; P:chemotaxis; IDA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 64 1 (POTENTIAL).
FT DOMAIN 65 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 95 2 (POTENTIAL).
FT DOMAIN 96 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 227 5 (POTENTIAL).
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 270 270 R -> S (IN REF. 2).
SQ SEQUENCE 359 AA; 41825 MW; AC11ED6E283CEAF CRC64;
Query Match 67.4%; Score 64; DB 1; Length 359;
Best Local Similarity 61.1%; Pred. No. 0.0016;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 YAFVGEKERNYLLVFFOK 18
Db 305 YAFVGEFRKHLRUFFFR 322

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RESULT 27
CCR3_RAT
ID CCR3_RAT STANDARD; PRT; 359 AA.
AC O54814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CCR-3) (CCR-3) (CCR3)
DE (CCR3).
GN CCR3 OR CMKBR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Spleen;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
RA Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
CC microglia.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF003954; AAC03337.1; -.
DR EMBL; Y13400; CAAT3830.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 1 (POTENTIAL).
FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 95 2 (POTENTIAL).
FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 3 (POTENTIAL).
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 227 5 (POTENTIAL).
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 264 6 (POTENTIAL).
FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 309 7 (POTENTIAL).
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 164 164 F -> L (IN REF. 2).
SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;
Query Match 67.4%; Score 64; DB 1; Length 359;

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Best Local Similarity 61.1%; Pred. No. 0.0016;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVCEKFRNVLVFFQK 18
DB 305 YAFVCEKFRNVLVFFQK 322

RESULT 28

CC CR8_HUMAN STANDARD; PRT; 355 AA.
AC P51685;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 8 (C-C CR8) (CC-CR8) (GPR-CY6)
DE (GPRCV6) (Chemokine receptor-like 1) (CCR-L1) (TER1) (CMKRL2) (CC-
DE chemokine receptor CHEMRL).
GN CR8 OR CMKRL2 OR CKRL1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351133; PubMed=9207005;
RA Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M.,
RA Combadiere C., Modi W., Bonner T.I., Murphy P.M.;
RT "Identification of CCR8: a human monocyte and thymus receptor for the
RT C-C chemokine I-309";
RL J. Exp. Med. 186:165-170 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98129363; PubMed=9469461;
RA Goya I., Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G.;
RT "Identification of CCR8 as the specific receptor for the human beta-
RT chemokine I-309: cloning and molecular characterization of murine
RT CCR8 as the receptor for TCA-3";
RL J. Immunol. 160:1975-1981 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97040707; PubMed=8886020;
RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;
RT "Molecular cloning and RNA expression of two new human chemokine
RT receptor-like genes";
RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97131825; PubMed=8977299;
RA Samson M., Stordeur P., Labbe O., Soularue P., Vassart G.,
RA Parmentier M.;
RT "Molecular cloning and chromosomal mapping of a novel human gene,
RT Chem1, expressed in T lymphocytes and polymorphonuclear cells and
RT encoding a putative chemokine receptor";
RL Eur. J. Immunol. 26:3021-3028 (1996).
RN [5]
RP SEQUENCE FROM N.A.
RX Nakajima T., Yoshida R., Harada S.;
RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP LIGAND BINDING.
RX MEDLINE=98180363; PubMed=9521068;
RA Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,
RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,
RA Napolitano M.;
RT "Identification of the C-C chemokines TARC and macrophage inflammatory
RT protein-1 beta as novel functional ligands for the CCR8 receptor";
RL Eur. J. Immunol. 28:582-588 (1998).
CC -1- FUNCTION: Receptor for the chemokines SCYA1/I-309, SCYA4/MIP-1-
CC beta and SCYA17/TARC. May regulate monocyte chemotaxis and thymic
CC cell line apoptosis. Alternative coreceptor with CD4 for HIV-1
CC infection.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: belongs to family 1 of G-protein coupled receptors.
CC
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CC EMBL; U45983; AAB61962.1; -
CC EMBL; U62556; AAB05542.1; -
CC EMBL; Z79782; CAB02142.1; -
CC EMBL; Y08456; CAA69712.1; -
CC EMBL; D49919; BAA23387.1; -
CC EMBL; AF005210; AAB62547.1; -
CC PIR; JC5067; JC5067.
CC Genew; HGNC:1609; CCR8.
CC MIM; 601834; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0004950; F: chemokine receptor activity; TAS.
CC GO; GO:0015026; F: coreceptor activity; TAS.
CC GO; GO:0007155; P: cell adhesion; TAS.
CC GO; GO:0006935; P: chemotaxis; TAS.
CC GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
CC GO; GO:0007186; P: G-protein coupled receptor protein signalin. . ; TAS.
CC GO; GO:0006955; P: immune response; TAS.
CC InterPro; IPR004068; CC 8 receptor.
CC InterPro; IPR000276; GPCR Rhodopsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR01530; CHEMOKINER8.
CC PRINTS; PR00237; GPCR RHODOPSIN.
CC PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC PROSITE; PS02462; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 35
FT EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 36 63
FT DOMAIN 64 73
FT CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 74 93
FT DOMAIN 94 107
FT EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 108 129
FT DOMAIN 130 146
FT CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 147 171
FT DOMAIN 172 202
FT EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 203 222
FT DOMAIN 223 238
FT CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 239 263
FT DOMAIN 264 280
FT EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 281 304
FT DOMAIN 305 355
FT CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183
FT BY SIMILARITY.
SQ SEQUENCE 355 AA; 40844 MW; BCI4A153CF695361 CRC64;

Query Match 66.3%; Score 63; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0024;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVCEKFRNVLVFFQK 18
DB 300 YAFVCEKFRNVLVFFQK 317

RESULT 29

CC CR8_MACMU STANDARD; PRT; 356 AA.
AC O97665;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 8 (C-C CR8) (CCR-8).
GN Macaca mulatta (Rhesus macaque).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=21354176; PubMed=11461684;
 RA Margulies B.J., Hauer D.A., Clements J.E.;
 RT "Identification and comparison of eleven rhesus macaque chemokine
 RT receptors";
 RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).
 CC -!- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY44/MIP-1-
 CC beta and SCY17/RAC. May regulate monocyte chemotaxis and thymic
 CC cell line apoptosis (by similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC -----
 DR EMBL; AF100205; AAC72403.1; -;
 DR InterPro; IPR004068; CC 8 receptor.
 DR InterPro; IPR00276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01530; CHEMOKINER8.
 DR PRINTS; PR0237; GPCRHOPOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECP FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 35
 FT TRANSMEM 36 63
 FT DOMAIN 64 73
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 74 93
 FT TRANSMEM 94 107
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 108 129
 FT TRANSMEM 130 146
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 147 172
 FT TRANSMEM 173 203
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 204 223
 FT TRANSMEM 224 239
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 240 264
 FT TRANSMEM 265 281
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 282 305
 FT TRANSMEM 306 356
 FT CYTOPLASMIC (POTENTIAL).
 FT DISULFID 106 184
 FT BY SIMILARITY.
 SQ SEQUENCE 356 AA; 41210 MW; 1979628DEE44845B CRC64;
 Query Match 66.3%; Score 63; DB 1; Length 356;
 Best Local Similarity 66.7%; Pred. No. 0.0024;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 YAFVGEKFRNVLVFFQK 18
 |||||:|:|
 Db 301 YAFVGEKFKHLSEIFQK 318
 RESULT 30
 CCR6_HUMAN
 ID CCR6_HUMAN STANDARD; PRT; 374 AA.
 AC P51684; P78553; Q92846;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE C-C chemokine receptor type 6 (C-C CKR-6) (CC-CCR-6) (CCR-6) (LARC
 DE receptor) (GPR-CV4) (GPCR4) (Chemokine receptor-like 3) (CCR-L3)
 DE (DRY6).
 GN CCR6 OR CXCR6 OR SREB22 OR GPR29 OR CXCR3.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.; AND FUNCTION.
 RX MEDLINE=97313465; PubMed=9169459;
 RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
 RA Nomiya H., Yoshie O.;
 RT "Identification of CCR6, the specific receptor for a novel
 RT lymphocyte-directed CC chemokine LARC";
 RL J. Biol. Chem. 272:14893-14898 (1997).
 CC [2]
 RN SEQUENCE FROM N.A.
 RA Lautens L.L., Modi W., Bonner T.I.;
 RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=886020;
 RA Zaballo A., Varona R., Gutierrez J., Lind P., Marquez G.;
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes";
 RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).
 CC [4]
 RN SEQUENCE FROM N.A.
 RA McCoy R., Perlmutter D.H.;
 RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97224503; PubMed=9070937;
 RA Liao F., Lee H.-H., Farber J.M.;
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6p27";
 RL Genomics 40:175-180 (1997).
 CC [6]
 RN SEQUENCE FROM N.A.
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 CC [7]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22935763; PubMed=14574404;
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Wilming L.J., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
 RA Chapman J.C., Clark S.V., Clark G., Clee C.M., Clegg S., Cobley V.,
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
 RA Cullen K.M., Dhali P., Davies J., Dunn M., Earthrowl M.E.,
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
 RA Gilby L.M., Gillson C.J., Griffiths R.J., Grafham D.V., Grant M.,
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLeay K.,
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
 RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
 RA Squares S.J., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
 RA Wall M., Wallis J.M., White A.P., White S.S., Whitehead S.L.,

RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 RA Durbin R., Hubbard T., Sulston J.B., Dunham I., Rogers J., Beck S.,
 RT "The DNA sequence and analysis of human chromosome 6";
 RL Nature 425:805-811(2003).
 RP [8]
 RN SEQUENCE FROM N.A.
 RC
 RX TISSUE=Pancreas;
 RA MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.I., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-
 alpha/LARC and subsequently transduces a signal by increasing the
 intracellular calcium ions level.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Spleen, lymph nodes, appendix, and fetal
 liver. Expressed in lymphocytes, T cells and B cells but not in
 natural killer cells, monocytes or granulocytes.
 CC -!- INDUCTION: By interleukin-2.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-6 is the initiator.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U45984; AAB62714.1; -;
 DR EMBL; Z79784; CAB02144.1; ALT_INIT.
 DR EMBL; U60000; AAB06949.1; -;
 DR EMBL; U68030; AAC51124.1; -;
 DR EMBL; U68032; AAC51125.1; -;
 DR EMBL; AY242126; AAC92293.1; -;
 DR EMBL; AL121935; CAB99328.1; -;
 DR EMBL; BC037960; AAB37960.1; -;
 DR HSSP; P34996; IDDD.
 DR Genew; HGNC:1607; CCR6.
 DR MIM; 601835; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. .); TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0006968; P:cellular defense response; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0006959; P:humoral immune response; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR004067; CC 6 receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR01529; CHEMOKINER6.

DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.
 DR PROSITE; PS0262; G PROTEIN RECP FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 74
 FT DOMAIN 75 83
 FT TRANSMEM 84 104
 FT DOMAIN 105 119
 FT TRANSMEM 120 141
 FT DOMAIN 142 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 211
 FT TRANSMEM 212 238
 FT DOMAIN 239 254
 FT TRANSMEM 255 279
 FT DOMAIN 280 303
 FT TRANSMEM 304 321
 FT DOMAIN 322 374
 FT DISULFID 118 197
 FT CARBOHYD 7 7
 FT CONFLICT 23 23
 FT CONFLICT 60 60
 FT CONFLICT 74 74
 FT CONFLICT 86 86
 FT CONFLICT 164 164
 FT CONFLICT 182 182
 FT CONFLICT 192 192
 FT CONFLICT 206 206
 FT CONFLICT 225 225
 FT CONFLICT 370 374
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;

Query Match 64.2%; Score 61; DB 1; Length 374;
 Best Local Similarity 76.3%; Pred. No. 0.0056;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
 |||:|:|:|:|
 Db 316 YAFIQKFRNYFL 328

Search completed: March 4, 2004, 18:00:07
 Job time : 6.07755 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 29.0204 Seconds
(without alignments)
195.701 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFRNLLVFFQX 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	333	4	O14694
2	95	100.0	334	6	Q9TU07
3	95	100.0	339	4	Q9UN24
4	95	100.0	339	4	Q9UN26
5	95	100.0	339	4	Q9UN23
6	95	100.0	339	4	Q9UBJ7
7	95	100.0	339	4	Q9UN25
8	95	100.0	339	4	Q9UN27
9	95	100.0	339	4	Q9UBT9
10	95	100.0	339	4	Q9UN28
11	95	100.0	339	6	Q9TQW0
12	95	100.0	339	6	Q9TUX1
13	95	100.0	339	6	Q9TUU9
14	95	100.0	339	6	Q9TUV8
15	95	100.0	339	6	Q9TUT4
16	95	100.0	339	6	Q9TUV9

Q9TSQ1 cercopithec
Q9TUN8 cercopithec
Q9TQW4 pan troglod
Q9TQW4 pan troglod
Q9TQW7 cercopithec
Q9TQW5 erythrocebu
Q9TUN3 macaca mula
Q9TUN9 saguinus sp
Q9TQW0 macaca fasc
Q9TUN9 macaca mula
Q9TUN2 macaca fasc
Q9TUN6 cercopithec
Q9TQW6 colobus que
Q9TUN6 pan troglod
Q9TUN9 cercopithec
Q9TUN3 macaca fasc
Q9TUN2 erythrocebu
Q9TUN7 macaca fusc
Q9TQW0 papio papio
Q9TUN6 macaca fusc
Q9TUN5 cercopithec
Q9TUN7 papio papio
Q9TUN7 pan troglod
Q9TUN3 pongo pygma
Q9TUN5 papio papio
Q9TUN0 macaca mula
Q9TQW2 papio papio
Q9TQW3 cercopithec
Q9TUN8 cercopithec
Q9TUN3 erythrocebu
Q9TQW2 pongo pygma
Q9TUN1 macaca mula
Q9TUN6 macaca neme
Q9TQX2 erythrocebu
Q9TUN4 mandrillus
Q9TQX3 mandrillus
Q9TUN5 alouatta ca
Q9TSQ4 cercopithec
Q9TUN3 macaca neme
Q9TUN0 macaca neme
Q9TQW2 gorilla gor
Q9TUN8 macaca mula
Q9TUN1 macaca neme
Q9TSQ3 cercopithec
Q9TUN0 cercopithec
Q9TUN5 pan troglod
Q9TQW4 erythrocebu
Q9TUN6 erythrocebu
Q9TQW2 macaca neme
Q9TQW1 macaca mula
Q9TUN5 macaca neme
Q9TUN8 papio papio
Q9TUN4 macaca mula
Q9TUN6 papio papio
Q9TUN7 cercopithec
Q9TQW4 cercopithec
Q9TUN6 cercopithec
Q9TUN7 macaca mula
Q9TUN0 hylobates c
Q9TSQ2 cercopithec
Q9TUN8 cercopithec
Q9TUN2 alouatta ca
Q9TUN5 macaca fusc
Q9TUN1 cercopithec
Q9TUN9 papio papio
Q9TUN2 macaca mula
Q9TUN8 cercocebu
Q9TQW3 cercocebu
Q9TSK1 cercopithec
Q9SNC5 hylobates s
Q9TUN48 cercopithec
Q9SNC4 ateles geof
Q9TUN9 cercocebu

17 95 100.0 339 6 Q9TSQ1
18 95 100.0 339 6 Q9TUN8
19 95 100.0 339 6 Q9TQW4
20 95 100.0 339 6 Q9TQW4
21 95 100.0 339 6 Q9TQW7
22 95 100.0 339 6 Q9TQW5
23 95 100.0 339 6 Q9TUN3
24 95 100.0 339 6 Q9TUN9
25 95 100.0 339 6 Q9TQW0
26 95 100.0 339 6 Q9TUN9
27 95 100.0 339 6 Q9TSN2
28 95 100.0 339 6 Q9TUN6
29 95 100.0 339 6 Q9TQW6
30 95 100.0 339 6 Q9TUN6
31 95 100.0 339 6 Q9TUN9
32 95 100.0 339 6 Q9TSN3
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39 95 100.0 339 6 Q9TUN7
40 95 100.0 339 6 Q9TUN3
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42 95 100.0 339 6 Q9TUN0
43 95 100.0 339 6 Q9TQW2
44 95 100.0 339 6 Q9TUN1
45 95 100.0 339 6 Q9TUT6
46 95 100.0 339 6 Q9TQX2
47 95 100.0 339 6 Q9TUN8
48 95 100.0 339 6 Q9TQW2
49 95 100.0 339 6 Q9TUN1
50 95 100.0 339 6 Q9TUT6
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52 95 100.0 339 6 Q9TUN4
53 95 100.0 339 6 Q9TQX3
54 95 100.0 339 6 Q9TUN5
55 95 100.0 339 6 Q9TSQ4
56 95 100.0 339 6 Q9TUT3
57 95 100.0 339 6 Q9TUT0
58 95 100.0 339 6 Q9TQW2
59 95 100.0 339 6 Q9TUT1
60 95 100.0 339 6 Q9TSQ3
61 95 100.0 339 6 Q9TUN0
62 95 100.0 339 6 Q9TUN5
63 95 100.0 339 6 Q9TQW4
64 95 100.0 339 6 Q9TQW6
65 95 100.0 339 6 Q9TQW2
66 95 100.0 339 6 Q9TQW1
67 95 100.0 339 6 Q9TUT5
68 95 100.0 339 6 Q9TUN8
69 95 100.0 339 6 Q9TUN4
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71 95 100.0 339 6 Q9TUN7
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85 95 100.0 339 6 Q9TSK1
86 95 100.0 339 6 Q9SNC5
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88 95 100.0 339 6 Q9SNC4
89 95 100.0 339 6 Q9TUN9

90 95 100.0 352 6 Q9XT14
 91 95 100.0 352 6 Q9XT76
 92 95 100.0 352 6 Q9SNC3
 93 95 100.0 352 6 Q9SNC3
 94 95 100.0 352 6 Q9TV47
 95 95 100.0 352 6 Q9SNC1
 96 95 100.0 352 6 Q9SNC1
 97 95 100.0 352 6 Q9SNC1
 98 95 100.0 352 6 Q9SNC6
 99 95 100.0 352 6 Q9SNC8
 100 95 100.0 352 6 Q9TV44

ALIGNMENTS

RESULT 1

O14694
 ID O14694 PRELIMINARY; PRT; 333 AA.
 AC O14694
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE CCR5 receptor (Fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
 RA Ho D.D.;
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).
 DR EMBL; AF011504; AAB65704.1; -;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS02362; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 333 333
 SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 95; DB 4; Length 333;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 Db 278 YAFVGEKFRNYLLVFFQK 295

RESULT 2

Q9TUQ7
 ID Q9TUQ7 PRELIMINARY; PRT; 334 AA.
 AC Q9TUQ7
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (fragment).
 GN CCR5.
 OS Erythrocybus pataas (Red guenon) (Hussar).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Erythrocybus.
 OX NCBI_TaxID=9538;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162049; AAD47804.1; -;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS02362; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 334 334
 SQ SEQUENCE 334 AA; 38460 MW; B19DOCEC667B69F0 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 334;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 Db 285 YAFVGEKFRNYLLVFFQK 302

RESULT 3

Q9UN24
 ID Q9UN24 PRELIMINARY; PRT; 339 AA.
 AC Q9UN24
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (fragment).
 GN CCR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161919; AAD47676.1; -;
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0004872; F: receptor activity; IEA.
 DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS02362; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 FT NON_TER 339 339
 SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 Db 290 YAFVGEKFRNYLLVFFQK 307

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RESULT 4
Q9UN26
ID Q9UN26 PRELIMINARY; PRT; 339 AA.
AC Q9UN26
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161916; AAD47673.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE052994AB CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
|||||
|||||

RESULT 5
Q9UN23
ID Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
|||||
|||||

RESULT 6
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFFF1F2F7A CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
|||||
|||||

RESULT 7
Q9UN25
ID Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
|||||
|||||

RESULT 6
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFFF1F2F7A CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
|||||
|||||

RESULT 7
Q9UN25
ID Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161918; AAD47675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
Db 290 YAFVGEKFRNLYLVFFQK 307

RESULT 8
Q9UN27 ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B4E2C84EC2 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
Db 290 YAFVGEKFRNLYLVFFQK 307

RESULT 9
Q9UBT9 ID Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29FA7 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18
Db 290 YAFVGEKFRNLYLVFFQK 307

RESULT 10
Q9UN28 ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
KW RECEPTOR.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 11
Q9TQW0
AC Q9TQW0 PRELIMINARY; PRT; 339 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161887; AAD47644.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
KW RECEPTOR.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 12
Q9TUX1
AC Q9TUX1 PRELIMINARY; PRT; 339 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161887; AAD47644.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
KW RECEPTOR.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39075 MW; 092577BFB834C4AE CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 13
Q9TUU9
AC Q9TUU9 PRELIMINARY; PRT; 339 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161948; AAD47704.1; -.
DR GO:00016021; C:integral to membrane; IEA.
DR GO:0004872; F:receptor activity; IEA.
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS50262; G-PROTEIN RECEPTOR FL2; 1.
KW RECEPTOR.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

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Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 14
ID Q9TUT8 PRELIMINARY; PRT; 339 AA.
AC Q9TUT8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 15
ID Q9TUT4 PRELIMINARY; PRT; 339 AA.
AC Q9TUT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 16
ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 17
ID Q9TSQ1 PRELIMINARY; PRT; 339 AA.

```

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species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; AAD47734.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 16
ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
   |||||
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 17
ID Q9TSQ1 PRELIMINARY; PRT; 339 AA.

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KW Receptor.
 FT NON TER 1
 FT NON TER 339
 SQ SEQUENCE 339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;

 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 DB 290 YAFVGEKFRNYLLVFFQK 307
 |||||

 RESULT 19
 Q9TQW4 PRELIMINARY; PRT; 339 AA.
 ID Q9TQW4
 AC Q9TQW4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 DE CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161905; AAD47662.1; -
 DR EMBL; AF161898; AAD47658.1; -
 DR EMBL; AF161901; AAD47658.1; -
 DR EMBL; AF161904; AAD47661.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCRHDOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 FT NON TER 1
 FT NON TER 339
 SQ SEQUENCE 339 AA; 39129 MW; 4A98F8BB601D46A4 CRC64;

 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 DB 290 YAFVGEKFRNYLLVFFQK 307
 |||||

 RESULT 20
 Q9TQW4 PRELIMINARY; PRT; 339 AA.
 ID Q9TQW4
 AC Q9TQW4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 DE CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161905; AAD47662.1; -
 DR EMBL; AF161898; AAD47658.1; -
 DR EMBL; AF161901; AAD47658.1; -
 DR EMBL; AF161904; AAD47661.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCRHDOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 FT NON TER 1
 FT NON TER 339
 SQ SEQUENCE 339 AA; 39129 MW; 4A98F8BB601D46A4 CRC64;

 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 DB 290 YAFVGEKFRNYLLVFFQK 307
 |||||

 RESULT 20
 Q9TQW4 PRELIMINARY; PRT; 339 AA.
 ID Q9TQW4
 AC Q9TQW4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 DE CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161905; AAD47662.1; -
 DR EMBL; AF161898; AAD47658.1; -
 DR EMBL; AF161901; AAD47658.1; -
 DR EMBL; AF161904; AAD47661.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCRHDOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 FT NON TER 1
 FT NON TER 339
 SQ SEQUENCE 339 AA; 39129 MW; 4A98F8BB601D46A4 CRC64;

 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
 DB 290 YAFVGEKFRNYLLVFFQK 307
 |||||

 RESULT 20
 Q9TQW4 PRELIMINARY; PRT; 339 AA.
 ID Q9TQW4
 AC Q9TQW4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C-C chemokine receptor 5 (Fragment).
 DE CCR5.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
 RT "Sequences of the CCR5 genes from diverse simian and prosimian
 RT species.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF161905; AAD47662.1; -
 DR EMBL; AF161898; AAD47658.1; -
 DR EMBL; AF161901; AAD47658.1; -
 DR EMBL; AF161904; AAD47661.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCRHDOPSN.
 DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW Receptor.
 FT NON TER 1
 FT NON TER 339
 SQ SEQUENCE 339 AA; 39129 MW; 4A98F8BB601D46A4 CRC64;

 Query Match 100.0%; Score 95; DB 6; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 YAFVGEK

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OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39159 MW; 8E699B882BAC0B84 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 21
Q9TUQ7 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecius.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03B6E2 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 22
Q9TUQ5 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162054; AAD47809.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307

RESULT 23
Q9TUU3 PRELIMINARY; PRT; 339 AA.
AC Q9TUU3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161961; AAD47716.1; -.

```

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DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39121 MW; AFB63EB4D6D3484 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
|||||

RESULT 24
Q9TUT9 ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162015; AAD4770.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
|||||

RESULT 25
Q9TUT9 ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162015; AAD4770.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
|||||

RESULT 26
Q9TUT9 ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161972; AAD4772.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.

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DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161954; AAD4770.1; -.
DR EMBL: AF161950; AAD47706.1; -.
DR EMBL: AF161952; AAD47708.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
|||||

RESULT 26
Q9TUT9 ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161972; AAD4772.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.

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FT  NON TER      1
FT  NON TER      339
SQ  SEQUENCE     339 AA, 39067 MW, 5BFCBC5BA96C2F9E CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNVLVFFQK 18
      |||||
DB      290 YAFVGEKFRNVLVFFQK 307

RESULT 27
Q9TSN2
ID  Q9TSN2      PRELIMINARY;      PRT;      339 AA.
AC  Q9TSN2;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Macaca fascicularis (Crab eating macaque) (Cynologus monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC  Cercopitheciinae; Macaca.
OX  NCBI_TaxID=9541;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species."
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF161953; AAD47709.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm 1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER      339
SQ  SEQUENCE     339 AA, 39178 MW, 9DF2AGF446C55AED CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNVLVFFQK 18
      |||||
DB      290 YAFVGEKFRNVLVFFQK 307

RESULT 28
Q9TUR6
ID  Q9TUR6      PRELIMINARY;      PRT;      339 AA.
AC  Q9TUR6;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Cercopithecus aethiops vervet.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC  Cercopitheciinae; Cercopithecus.
OX  NCBI_TaxID=100936;
RN  [1]

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RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species."
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF162026; AAD47781.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm 1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER      339
SQ  SEQUENCE     339 AA, 39178 MW, 9DF2AGF446C55AED CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNVLVFFQK 18
      |||||
DB      290 YAFVGEKFRNVLVFFQK 307

RESULT 29
Q9TOV6
ID  Q9TOV6      PRELIMINARY;      PRT;      339 AA.
AC  Q9TOV6;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  C-C chemokine receptor 5 (Fragment).
GN  CCR5.
OS  Colobus quereza (Black-and-white colobus monkey).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae; Colobinae;
OC  Colobus.
OX  NCBI_TaxID=33548;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA  Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT  "Sequences of the CCR5 genes from diverse simian and prosimian
RT  species."
RL  Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF162005; AAD47760.1; -.
DR  EMBL; AF162000; AAD47755.1; -.
DR  EMBL; AF162001; AAD47756.1; -.
DR  EMBL; AF162002; AAD47757.1; -.
DR  EMBL; AF162003; AAD47758.1; -.
DR  EMBL; AF162004; AAD47759.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  Pfam; PF00001; 7tm 1; 1.
DR  PRINTS; PR00237; GPCRHHODPSN.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
FT  NON TER      1
FT  NON TER      339
SQ  SEQUENCE     339 AA, 39168 MW, 6A43F72FBBFF566F CRC64;

Query Match      100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 290 YAFVGEKFRNLLVFFQK 307

RESULT 30

Q9TUM6 PRELIMINARY; PRT; 339 AA.
AC Q9TUM6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kiiken C., Marx P., Wolinsky S.;
RT "sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF161900; AAD47657.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39103 MW; 4038CL32D024C5A4 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;

Best Local Similarity 100.0%; Pred. No. 1.le-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 290 YAFVGEKFRNLLVFFQK 307

Search completed: March 4, 2004, 18:02:56

Job time : 29.0204 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	95	100.0	352	3	US-08-466-343D-13		Sequence 2, Appli
2	95	100.0	352	3	US-09-087-232A-13		Sequence 13, Appl
3	95	100.0	352	3	US-08-861-105-14		Sequence 14, Appl
4	95	100.0	352	3	US-08-575-967A-2		Sequence 2, Appli
5	95	100.0	352	3	US-08-045-583-52		Sequence 52, Appl
6	95	100.0	352	4	US-09-517-605-5		Sequence 5, Appli
7	95	100.0	352	4	US-09-534-185-52		Sequence 52, Appl
8	95	100.0	352	4	US-08-833-752-5		Sequence 5, Appli
9	95	100.0	352	4	US-09-502-783A-2		Sequence 2, Appli
10	95	100.0	352	4	US-09-796-202-1		Sequence 1, Appli
11	80	84.2	354	4	US-08-724-984A-2		Sequence 2, Appli
12	79	83.2	347	1	US-08-461-244-3		Sequence 3, Appli
13	79	83.2	360	1	US-08-450-393A-4		Sequence 4, Appli
14	79	83.2	360	3	US-08-446-669-4		Sequence 4, Appli
15	79	83.2	360	3	US-09-045-583-50		Sequence 50, Appl
16	79	83.2	360	4	US-09-534-185-50		Sequence 50, Appl
17	79	83.2	360	4	US-09-131-827A-2		Sequence 2, Appli
18	79	83.2	360	4	US-09-131-827A-20		Sequence 20, Appl
19	79	83.2	360	5	PCT-US95-00476-4		Sequence 4, Appli
20	77	81.1	360	4	US-08-833-752-7		Sequence 7, Appli
21	76	80.0	360	3	US-09-045-583-51		Sequence 51, Appl
22	76	80.0	360	4	US-09-534-185-51		Sequence 51, Appl
23	65	68.4	355	3	US-08-575-967A-4		Sequence 4, Appli
24	65	68.4	355	3	US-08-847-296B-1		Sequence 1, Appli
25	65	68.4	355	3	US-09-045-583-54		Sequence 54, Appl
26	65	68.4	355	4	US-09-534-185-54		Sequence 54, Appl
27	65	68.4	355	4	US-08-720-565-2		Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LL, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 2

US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Qullent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-087-232A-13

Query Match 100.0%; Score 95; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314
|||||

RESULT 3

US-08-861-105-14
; Sequence 14, Application US/08861105
; Patent No. 6258527
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; APPLICANT: DENG, HONGKUI
; APPLICANT: ELLMEIER, WILFRIED
; APPLICANT: LANDAU, NATHANIEL R.
; APPLICANT: LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,105
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1049-1-004 N1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-861-105-14

Query Match 100.0%; Score 95; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.2e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 4
 US-08-575-967A-2
 ; Sequence 2, Application US/08575967A
 ; Patent No. 6265184
 ; GENERAL INFORMATION:
 ; APPLICANT: Gray et al.
 ; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 S. Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/575,967A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6265184 and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 32918
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-485-1662
 ; TELEFAX: 206-485-1662
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: /= "88C amino acid sequence"
 US-08-575-967A-2

Query Match 100.0%; Score 95; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.2e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18

Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 5
 US-09-045-583-52
 ; Sequence 52, Application US/09045583
 ; Patent No. 6287805
 ; GENERAL INFORMATION:
 ; APPLICANT: Graham, Gerard J. et al.
 ; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/045,583
 ; FILING DATE: 20-MAR-98
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragouras, Amy E.
 ; REGISTRATION NUMBER: 36,207
 ; REFERENCE/DOCKET NUMBER: MNI-044
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 52:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 352 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 ; US-09-045-583-52

Query Match 100.0%; Score 95; DB 3; Length 352;
 Best Local Similarity 100.0%; Pred. No. 8.2e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 6
 US-09-517-605-5
 ; Sequence 5, Application US/09517605
 ; Patent No. 6391567
 ; GENERAL INFORMATION:
 ; APPLICANT: Kwon, Douglas S.
 ; APPLICANT: Kwon, Douglas S.
 ; APPLICANT: van Kooyk, Yvette
 ; APPLICANT: Geijtenbeek, Theo
 ; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
 ; TITLE OF INVENTION: CELLS
 ; FILE REFERENCE: 1049-1-017
 ; CURRENT APPLICATION NUMBER: US/09/517,605
 ; CURRENT FILING DATE: 2000-03-02
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 5

; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-5

Query Match 100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 7

US-09-534-185-52
; Sequence 52, Application US/09534185
; Patent No. 6403767

GENERAL INFORMATION:

APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-534-185-52

Query Match 100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 8

US-08-833-752-5
; Sequence 5, Application US/08833752
; Patent No. 6448375

GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-752-5

Query Match 100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 9

US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. 6511826

GENERAL INFORMATION:

APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR
TITLE OF INVENTION: HDGR10
FILE REFERENCE: 1488.1150006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
|||||

Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 10

US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JFW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 95; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 11

US-08-724-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6388055
; GENERAL INFORMATION:
; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon
; TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
; TITLE OF INVENTION: CCR5 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,984A
FILING DATE: October 3, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han

REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
TELEFAX: 610 270 5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 354
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-724-984A-2

Query Match 84.2%; Score 80; DB 4; Length 354;
Best Local Similarity 83.3%; Pred. No. 3.5e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

Db 299 YAFVGEKFRNLLVFFQK 316

RESULT 12

US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,244
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-244-3

Query Match 83.2%; Score 79; DB 1; Length 347;
Best Local Similarity 83.3%; Pred. No. 5.2e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

Db 292 YAFVGEKFRNLLVFFQK 309

RESULT 13

US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Cooley Godward Castro Huddleson & Tatum
FILING DATE: May 25, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: UCAL-237/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
TELEFAX: 415-857-0663
TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 83.2%; Score 79; DB 1; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFOK 18
|||||

Db 305 YAFVGEKFRNLLVFFOK 322

RESULT 14
US-08-446-669-4
Sequence 4, Application US/08446669
Patent No. 6132987
GENERAL INFORMATION:
APPLICANT: Charo, Israel
APPLICANT: Coughlin, Shaun
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Cooley Godward Castro Huddleson & Tatum
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663

TELEX: 380816CooleyPA
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-669-4

Query Match 83.2%; Score 79; DB 3; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFOK 18
|||||

Db 305 YAFVGEKFRNLLVFFOK 322

RESULT 15
US-09-045-583-50
Sequence 50, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Cooley Godward Castro Huddleson & Tatum
FILING DATE: May 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-237/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663

Query Match 83.2%; Score 79; DB 3; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFOK 18
|||||

Db 305 YAFVGEKFRNLLVFFOK 322

RESULT 16
US-09-534-185-50
Sequence 50, Application US/09534185

Patent No. 6403767
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50
Query Match 83.2%; Score 79; DB 4; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
Db 305 YAFVGEKFRNYLLVFFRK 322
RESULT 17
US-09-131-827A-2
Sequence 2, Application US/09131827A
Patent No. 6600030
GENERAL INFORMATION:
APPLICANT: Dean, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
FILE REFERENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 360
TYPE: PRT
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

ORGANISM: Homo sapiens
US-09-131-827A-2
Query Match 83.2%; Score 79; DB 4; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
Db 305 YAFVGEKFRNYLLVFFRK 322
RESULT 18
US-09-131-827A-20
Sequence 20, Application US/09131827A
Patent No. 6600030
GENERAL INFORMATION:
APPLICANT: Dean, Michael
APPLICANT: O'Brien, Stephen J.
APPLICANT: Smith, Michael
APPLICANT: Carrington, Mary
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
FILE REFERENCE: 14014.0333
CURRENT APPLICATION NUMBER: US/09/131,827A
CURRENT FILING DATE: 1998-08-10
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-131-827A-20
Query Match 83.2%; Score 79; DB 4; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
Db 305 YAFVGEKFRNYLLVFFRK 322
RESULT 19
PCT-US95-00476-4
Sequence 4, Application PC/TUS9500476
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
TITLE OF INVENTION: PROTEIN RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 N. Figueroa Street, 5th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00476
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-291

TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-977-1001
TELEFAX: 310-977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00476-4

Query Match 83.2%; Score 79; DB 5; Length 360;
Best Local Similarity 83.3%; Pred. No. 5.4e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 305 YAFVGEKFRNVLVFFQK 322

RESULT 20

US-08-833-752-7
Sequence 7, Application US/08833752
Patent No. 6448375

GENERAL INFORMATION:
APPLICANT: SAMSON, MICHEL
APPLICANT: PARMENTIER, MARC
APPLICANT: VASSART, GILBERT
APPLICANT: LIBERT, FREDERICK
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,752
FILING DATE: 9-APR-1997
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match 81.1%; Score 77; DB 4; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.2e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 305 YAFVGEKFRNVLVFFQK 322

RESULT 21

US-09-045-583-51

Sequence 51, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: NO. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-045-583-51

Query Match 80.0%; Score 76; DB 3; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18
Db 305 YAFVGEKFRNVLVFFQK 322

RESULT 22

US-09-534-185-51
Sequence 51, Application US/09534185
Patent No. 6403767

GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
Heptahelical Receptor Superfamily and Uses
Therefor

NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185
FILING DATE: 24-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/045,583
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-534-185-51

Query Match 80.0%; Score 76; DB 4; Length 360;
Best Local Similarity 77.8%; Pred. No. 1.8e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 305 YAFVGEKFRYLSNFFRK 322

RESULT 23
US-08-575-967A-4
Sequence 4, Application US/08575967A
Patent No. 6265184
GENERAL INFORMATION:
APPLICANT: Gray et al.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: /= "88-2B amino acid sequence"
US-08-575-967A-4

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 301 YAFVGERFRKYLRRHFHR 318

RESULT 24
US-08-847-296B-1
Sequence 1, Application US/08847296B
Patent No. 6271347
GENERAL INFORMATION:
APPLICANT: DAUGHERTY, BRUCE L.
APPLICANT: DEMARTINO, JULIE A.
APPLICANT: SICILIANO, SALVATORE J.
APPLICANT: SPRINGER, MARTIN J.
TITLE OF INVENTION: EOSINOPHIL ROTAXIN RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,296B
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,158
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 60/017,113
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Thies, J. Eric
REGISTRATION NUMBER: 35,382
REFERENCE/DOCKET NUMBER: 19634Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3904
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-847-296B-1

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 301 YAFVGERFRKYLRRHFHR 318

RESULT 25
US-09-045-583-54
Sequence 54, Application US/09045583
Patent No. 6287805
GENERAL INFORMATION:

```

; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-54

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 301 YAFVGERPKYLRHFFHR 318

RESULT 26
US-09-534-185-54
; Sequence 54, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Hepatocellular Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>

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```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-534-185-54

Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 301 YAFVGERPKYLRHFFHR 318

RESULT 27
US-08-720-565-2
; Sequence 2, Application US/08720565
; Patent No. 6537764
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; APPLICANT: Gerard, No. 6537764ma P.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STANDARDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-720-565-2

Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
|||||:|||||:
DB 301 YAFVGEKFRNYLLVFFQK 318

RESULT 28

US-08-720-565-4
Sequence 4, Application US/08720565
Patent No. 6537764

GENERAL INFORMATION:

APPLICANT: Gerard, Craig J.
APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Post, Theodore W.
APPLICANT: Qin, Shixin

TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
TITLE OF INVENTION: ANTAGONISTS THEREOF

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/720,565

FILING DATE: 30-SEP-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00608

FILING DATE: 19-JAN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/375,199

FILING DATE: 19-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: LKS94-05A2

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 355 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-720-565-4

Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18

DB 301 YAFVGEKFRNYLLVFFQK 318
|||||:|||||:
|||:

RESULT 29

US-08-567-882-7

Sequence 7, Application US/08567882

Patent No. 6512103

GENERAL INFORMATION:

APPLICANT: Dairaghi, Daniel J.

APPLICANT: Hara, Takahiko

APPLICANT: Miyajima, Atsushi

APPLICANT: Schall, Thomas J.

APPLICANT: Wang, Wei

APPLICANT: Yoshimura, Akihiko

TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/567,882

FILING DATE: 08-DEC-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0506

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 356 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-567-882-7

Query Match 68.4%; Score 65; DB 4; Length 356;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18

|||||:|||||:
|||:

DB 302 YAFVGEKFRNYLLVFFQK 319

RESULT 30

US-08-461-244-2

Sequence 2, Application US/08461244

Patent No. 5776729

GENERAL INFORMATION:

APPLICANT: Soppet, Daniel R.

APPLICANT: Yi, Li

APPLICANT: Ruben, Steven M.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

ADDRESSEE: STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland


```

; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-2

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Query Match      66.3%; Score 63; DB 1; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0034;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
Db 300 YAFVGEKFKHLSEIFQK 317

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Search completed: March 4, 2004, 18:05:15
Job time : 11.5714 secs

Sequence 9, Appli
Sequence 2, Appli
Sequence 78, Appli
Sequence 2, Appli
Sequence 40, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 130, App
Sequence 232, App
Sequence 249, App

ALIGNMENTS

RESULT 1
US-10-084-813-15
; Sequence 15, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-15

Query Match 100.0%; Score 95; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 1 YAFVGEKFRNLLVFFQK 18

RESULT 2
US-10-084-813-105
; Sequence 105, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-105

Query Match 100.0%; Score 95; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 1 YAFVGEKFRNLLVFFQK 18

RESULT 3
US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030148294A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Bandman, Olga
; APPLICANT: Coleman, Roger; Wilde, Craig G.
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
; FILE REFERENCE: PF-0060-1 CON
; CURRENT APPLICATION NUMBER: US/10/095,876A
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 08/638,081
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

Query Match 100.0%; Score 95; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 277 YAFVGEKFRNLLVFFQK 294

RESULT 4
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGKR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 5
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Petros, Manousos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 6
US-09-779-879A-2
; Sequence 2, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 7
US-09-779-879A-22
; Sequence 22, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-22

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 8
US-09-779-880A-2
; Sequence 2, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-2

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 9
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 10
US-09-813-653-15
; Sequence 15, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-15

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 11
US-09-813-653-17
; Sequence 17, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-653-17

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 12
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
| | | | | | | | | | | | | | | | | |
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 13
US-09-195-662A-2
; Sequence 2, Application US/09195662A
; Patent No. US20020076745A1

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;
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGRL10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
; US-09-195-662A-2

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 14
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGRL10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
; US-09-339-912A-2

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 15
US-09-338-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
```

```
;
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-09-938-719-5

Query Match      100.0%; Score 95; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YAFVGEKFRNYLLVFFQK 18
      |||||
Db      297 YAFVGEKFRNYLLVFFQK 314

RESULT 16
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
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1 FILING DATE: 2000-07-27
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Altman, Daniel E
4 REGISTRATION NUMBER: 34,115
5 REFERENCE/DOCKET NUMBER: <Unknown>
6 INFORMATION FOR SEQ ID NO: 5:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 352 amino acids
9 TYPE: amino acid
10 TOPOLOGY: linear
11 MOLECULE TYPE: protein
12 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
13 US-09-938-703-5
14
15 Query Match 100.0%; Score 95; DB 9; Length 352;
16 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
17 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
18
19 QY 1 YAFVGEKFRNYLLVFFQK 18
20 |||||
21 Db 297 YAFVGEKFRNYLLVFFQK 314
22
23 RESULT 17
24 US-09-938-703-5
25 ; Sequence 5, Application US/09938703
26 ; Patent No. US20020110870A1
27 ; GENERAL INFORMATION:
28 ; APPLICANT: SAMSON, MICHEL
29 ; PARENTIER, MARC
30 ; VASSART, GILBERT
31 ; LIBERT, FREDERICK
32 ; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
33 ; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
34 ;
35 ; NUMBER OF SEQUENCES: 17
36 ; CORRESPONDENCE ADDRESS:
37 ; ADDRESSEE: Knobbe, Martens, Olson & Bear
38 ; STREET: 620 Newport Center Drive 16th Floor
39 ; CITY: Newport Beach
40 ; STATE: CA
41 ; COUNTRY: U.S.A.
42 ; ZIP: 92660
43 ; COMPUTER READABLE FORM:
44 ; MEDIUM TYPE: Floppy disk
45 ; COMPUTER: IBM PC compatible
46 ; OPERATING SYSTEM: PC-DOS/MS-DOS
47 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
48 ; CURRENT APPLICATION DATA:
49 ; APPLICATION NUMBER: US/09/938,703
50 ; FILING DATE: 24-Aug-2001
51 ; CLASSIFICATION: <Unknown>
52 ; PRIOR APPLICATION DATA:
53 ; APPLICATION NUMBER: 09/626,939
54 ; FILING DATE: 2000-07-27
55 ; ATTORNEY/AGENT INFORMATION:
56 ; NAME: Altman, Daniel E
57 ; REGISTRATION NUMBER: 34,115
58 ; REFERENCE/DOCKET NUMBER: <Unknown>
59 ; INFORMATION FOR SEQ ID NO: 5:
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 352 amino acids
62 TYPE: amino acid
63 TOPOLOGY: linear
64 MOLECULE TYPE: protein
65 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
66 US-09-938-703-5
67
68 Query Match 100.0%; Score 95; DB 9; Length 352;
69 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
70 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
71
72 QY 1 YAFVGEKFRNYLLVFFQK 18
73 |||||
74 Db 297 YAFVGEKFRNYLLVFFQK 314
75
76 RESULT 18
77 US-09-502-783A-2
78 ; Sequence 2, Application US/09502783A
79 ; Patent No. US20020132269A1
80 ; GENERAL INFORMATION:
81 ; APPLICANT: Li, Yi
82 ; APPLICANT: Ruben, Steven M.
83 ; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR)
84 ; TITLE OF INVENTION: HDGNR10
85 ; FILE REFERENCE: 1488.1150006
86 ; CURRENT APPLICATION NUMBER: US/09/502,783A
87 ; CURRENT FILING DATE: 2001-08-23
88 ; PRIOR APPLICATION NUMBER: 08/466,343
89 ; PRIOR FILING DATE: 1995-06-06
90 ; NUMBER OF SEQ ID NOS: 9
91 ; SOFTWARE: Patentin version 3.0
92 ; SEQ ID NO 2
93 ; LENGTH: 352
94 ; TYPE: PRT
95 ; ORGANISM: Homo sapiens
96 ; US-09-502-783A-2
97
98 Query Match 100.0%; Score 95; DB 9; Length 352;
99 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
100 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
101
102 QY 1 YAFVGEKFRNYLLVFFQK 18
103 |||||
104 Db 297 YAFVGEKFRNYLLVFFQK 314
105
106 RESULT 19
107 US-09-734-221A-14
108 ; Sequence 14, Application US/09734221A
109 ; Publication No. US20030096221A1
110 ; GENERAL INFORMATION:
111 ; APPLICANT: LITTMAN, DAN R.
112 ; DENG, HONGKUI
113 ; ELMEIER, WILFRIED
114 ; LANDAU, NATHANIEL R.
115 ; LIU, RONG
116 ; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
117 ; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
118 ; USES THEREOF
119 ;
120 ; NUMBER OF SEQUENCES: 14
121 ; CORRESPONDENCE ADDRESS:
122 ; ADDRESSEE: David A. Jackson, Esq.
123 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
124 ; Floor
125 ; CITY: Hackensack
126 ; STATE: New Jersey
127 ; COUNTRY: USA
128 ; ZIP: 07601
129 ; COMPUTER READABLE FORM:
130 ; MEDIUM TYPE: Floppy disk
131 ; COMPUTER: IBM PC compatible
132 ; OPERATING SYSTEM: PC-DOS/MS-DOS
133 ; SOFTWARE: Patentin Release #1.0, Version #1.30
134 ; CURRENT APPLICATION DATA:
135 ; APPLICATION NUMBER: US/09/734,221A
136 ; FILING DATE: 11-Dec-2000
137 ; CLASSIFICATION: <Unknown>
138 ; PRIOR APPLICATION DATA:
139 ; APPLICATION NUMBER: US 08/666,020
140 ; FILING DATE: 19-JUN-1996
141 ; APPLICATION NUMBER: US 08/227,319
142 ; FILING DATE: 13-APR-1994
143 ; ATTORNEY/AGENT INFORMATION:
144 ; NAME: Jackson Esq., David A.
145 ; REGISTRATION NUMBER: 26,742

```
/
/ REFERENCE/DOCKET NUMBER: 1049-1-004 N2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 352 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

Query Match 100.0%; Score 95; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 20
US-09-826-509-477
/ Sequence 477, Application US/09826509
/ Publication No. US20030204073A1
/ GENERAL INFORMATION:
/ APPLICANT: Lehmann-Bruinsma, Karin
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
/ TITLE OF INVENTION: Protein-Coupled Receptors
/ FILE REFERENCE: AREN-207
/ CURRENT APPLICATION NUMBER: US/09/826,509
/ CURRENT FILING DATE: 2001-04-05
/ PRIOR APPLICATION NUMBER: 60/195,747
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 589
/ SOFTWARE: PatentIn Version 2.1
/ SEQ ID NO 477
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-826-509-477

Query Match 100.0%; Score 95; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 21
US-10-106-623-2
/ Sequence 2, Application US/10106623
/ Publication No. US20020150888A1
/ GENERAL INFORMATION:
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schweickart, Vicky L.
/ APPLICANT: Report, Carol J.
/ TITLE OF INVENTION: Chemokine Receptor Materials and Methods
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
```

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/
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/106,623
/ FILING DATE: 26-Mar-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/771,276
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. US20020150888A1and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/33670
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 352 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: /= "88C amino acid sequence"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 100.0%; Score 95; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 22
US-10-106-623-20
/ Sequence 20, Application US/10106623
/ Publication No. US20020150888A1
/ GENERAL INFORMATION:
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: Schweickart, Vicky L.
/ APPLICANT: Report, Carol J.
/ TITLE OF INVENTION: Chemokine Receptor Materials and Methods
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/106,623
/ FILING DATE: 26-Mar-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/771,276
/ FILING DATE: <Unknown>
```


ATTORNEY/AGENT INFORMATION:
NAME: No. US20020150888aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-106-623-20

Query Match 100.0%; Score 95; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 23
US-10-232-686-2
Sequence 2, Application US/10232686
Publication No. US20030023044A1
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000N
CURRENT APPLICATION NUMBER: US/10/232,686
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 09/339,912
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/466,343
PRIOR FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-232-686-2

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 24
US-10-086-814-1
Sequence 1, Application US/10086814
Publication No. US20030092632A1
GENERAL INFORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William C.
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REFERENCE: 61010-AB-1
CURRENT APPLICATION NUMBER: US/10/086,814
CURRENT FILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patent in version 3.1
SEQ ID NO 1

LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 25
US-10-067-800-2
Sequence 2, Application US/10067800
Publication No. US20030100058A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000I
CURRENT APPLICATION NUMBER: US/10/067,800
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: PCT/US01/04153
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/779,880
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/297,257
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/310,458
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/328,447
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/341,725
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patent in version 3.1
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Homo sapiens
US-10-067-800-2

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 26
US-10-067-800-22
Sequence 22, Application US/10067800
Publication No. US20030100058A1
GENERAL INFORMATION:
APPLICANT: Roschke, Viktor
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven, M.
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
FILE REFERENCE: 1488.115000I
CURRENT APPLICATION NUMBER: US/10/067,800
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: PCT/US01/04153
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/779,880
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/297,257
PRIOR FILING DATE: 2001-06-12

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 352
 ; LENGTH: 352
 ; TYPE: PRT

Search completed: March 4, 2004, 18:22:53
Job time : 24.0612 secs